

FIG. 1A

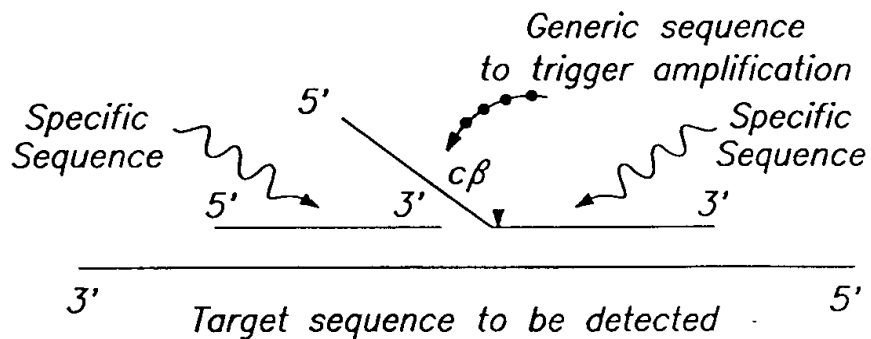


FIG. 1B PART ONE: TRIGGER REACTION

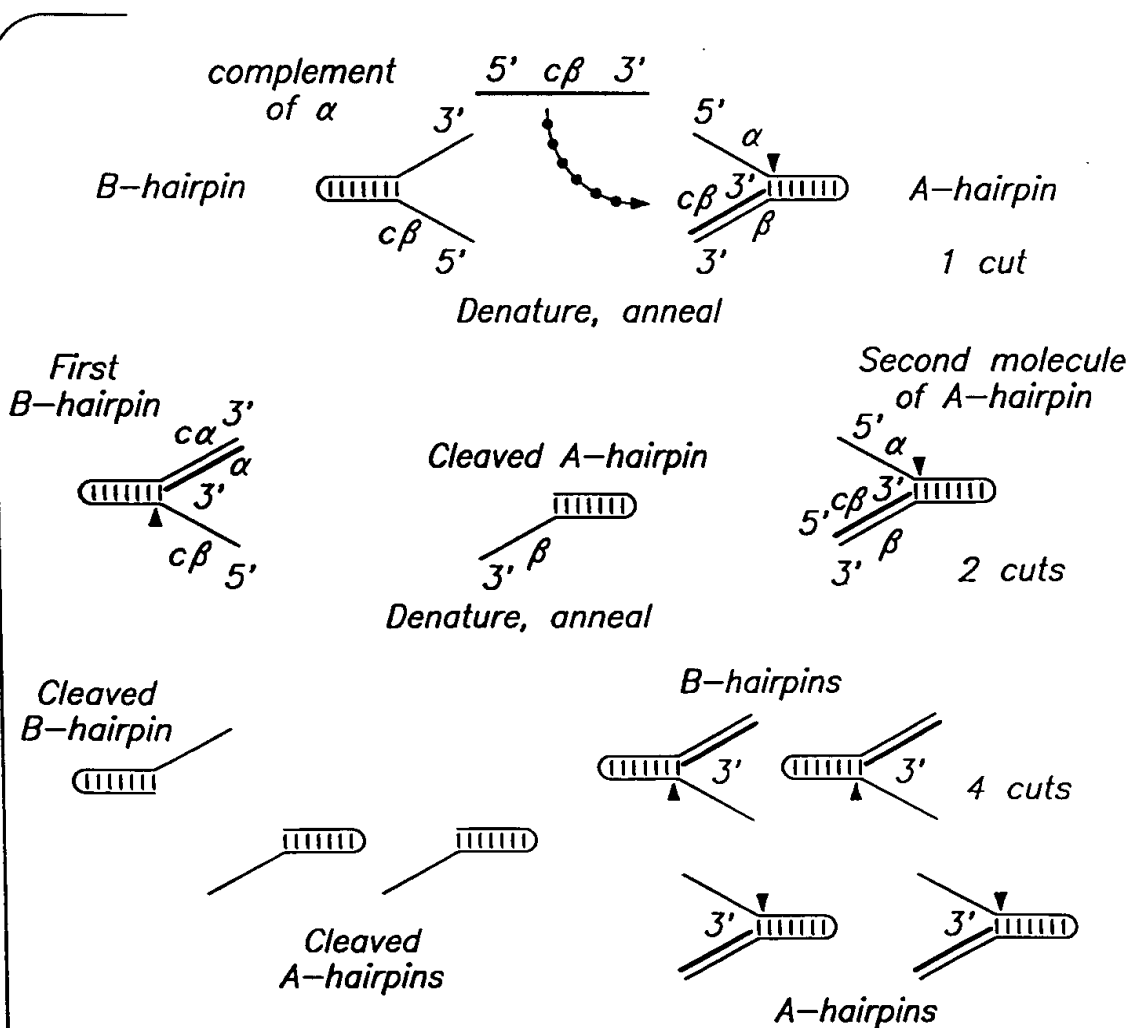


FIG. 1C PART TWO: DETECTION REACTION

09982667-101801

MAJORITY	ATGXXGGCGATGCTTCCCTCTTTGAGCCAAAGGCCGGTCTCCTGTTGGACGGGCACCTGGCCT	
DNAPTAQ	...AG..G.....G.....	70
DNAPTFLC..G.....	67
DNAPTTH	...GA.....G.....A.....	70
MAJORITY	ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCACCGGGGGAACCGGTGCAGGGCGGTCTACGGCTT	
DNAPTAQCA.....G..G.....	140
DNAPTFLT.....C.....C..T.....	137
DNAPTTHG.....	140
MAJORITY	CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGCCGGTGXTCTGTTGACGCCAAG	
DNAPTAQC.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	280
MAJORITY	GCCCCCTCCTTCGCGCCACGAGGCCCTACGAGGCCCTACAAGCGGGCGGCCCCACCCCGGAGGACTTTC	
DNAPTAQG..GG.....G.....	277
DNAPTFLGA.....G.....C.....	274
DNAPTTHGA.....G.....C.....	280
MAJORITY	CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGCGGCGCCTCGAGGTCCCCGGCTA	
DNAPTAQA.....G.....G.....G.....	347
DNAPTFLG.....T.....A..C.....T..G..G.....T.....	344
DNAPTTHT.....T..A.C.....	350

FIG. 2A

MAJORITY	CGAGGCGGACGACGTXCTGGCCACCTGGCCAGAAGGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC	
DNAPTAQC.....G.....C.....C.....	417
DNAPTFL	T.....G.....CG.....	414
DNAPTTHT.C.....	420
MAJORITY	ACGCGGACCGGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G.....G.....A.....T.....G.	484
DNAPTTHA..G.C.....G.....CC.....	490
MAJORITY	TCACCCCGCGGTGGCTTTGGGAGAAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC	
DNAPTAQC.....A.....C..C.....CC.....A.	557
DNAPTFLAC.....C.C.....T..C.....C.T	554
DNAPTTH	A.....C.....	560
MAJORITY	GGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAAAGACCGCCXGAAGCTCCTCXAG	
DNAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFLG..T..A.....G.....A..G...A..CGC	624
DNAPTTHTC.....A..	630
MAJORITY	GAGTGGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCCG...XTCCGGGGAGAAGA	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..C..C.....A.....T.....T.G.....C	691
DNAPTTHA.....A.....A.AAA.G.....	700

FIG. 2B

MAJORITY	TCCAGGCCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCACAGGTGGCGCACCGACCTGCCCTGGCA
DNAPTAQ	...T.....C..T...A.....C..GG..A.....
DNAPTFL	...GGG.....G.C...GCC.T...C..A...T.....A...T.....
DNAPTTH	..A.....C.....A.....C.G.....T.....C.....G.....C.....
MAJORITY	GGTGGACTTCGCCAAGXGGCGGGAGCCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT
DNAPTAQAA.....A.....A.....A.....T.....T.....T.....
DNAPTFLGG.G.C.C..CACA...A...T.....T..GC...T...T...C..T.....
DNAPTTHC.....C..G.....C.....C.....C.....C.....C.....C.....
MAJORITY	GGCAGCCTCCTCCACGAGTTTCGGCCTCCTGGAGGGGCCCCAAGGCCCTGGAGGAGGCCCTGGCCCCCGC
DNAPTAQT.....AA.....
DNAPTFL	..A.....DNAPTFL.....G..G.....GGCA.....T..
DNAPTTHC.....GCCC.....
MAJORITY	CGGAAGGGGCTTCGTGGGCTTTGTCTCTTTCCCGCCCCGAGCCCCATGTGGGCCGAGCTTCTGGCCCCCTGGC
DNAPTAQG.....AAG.....T.....
DNAPTFLT..TT.....TC.T.....T.....
DNAPTTHC.....C.....G.....AAA.....
MAJORITY	CGCCGCCAGGAGGGCCGGTCCACCGGCACACACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG
DNAPTAQG.....C..C..G..T.A..AA.C...C.....G.....C.....
DNAPTFL	T.GG..GT.....G..CC...T.....A.....C...G.....G.....T.....G.....
DNAPTTHTG.....C.....G.....G.....GGC...G..A..A.....C.....C.....

1

MAJORITY	CGGGXCTCCTCGCCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGCCTXGACCTCXTGCCCGGGGACG	
DNAPTAQG..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFLAA.....G.....C.....C.....G.....T.C..A.A.....	1111
DNAPTTHC.....C.....TC.....G.A.....G.....G.....	1120
MAJORITY	ACCCCATGCTCCTCGCTACCTCCTGGACCCCTCCAACACCACCCCGAGGGGTGGCCCCGGCGCTACGG	
DNAPTAQG.....T.....T.....T.....T.....T.....	1184
DNAPTFLG.....T.....T.....T.....T.....T.....	1181
DNAPTTHG.....T.....T.....T.....T.....T.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXGGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GCC.....GTG...G.	1254
DNAPTFLT.....A.....GG.....C.C.....A..C...AAA....	1260
DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGAGGAGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCTTTCCCGGGTCCIGG	
DNAPTAQ	A.G.....G.....G.....G.....G.....GCT.....	1324
DNAPTFLA...A..A..AC.C.G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA	
DNAPTAQG.C.....G.C.....T...AG.....T.G.....C...	1394
DNAPTFLGG.....C.....C.....T.....C.....A..C	1391
DNAPTTHC.....A.....A.....T.....T.....C.T.....	1400

FIG.2D

MAJORITY	GGAGATCCGCCCGCCTCGAGGAGGAGGTCTTCCGGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCCGGGAC	
DNAPTAQGC.....CC.....	1464
DNAPTFLG.G....AG..G.....	1461
DNAPTTHT.....G.....	1470
MAJORITY	CAGCTGGAAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAAGACXGGCAAGC	
DNAPTAQC.....A.....	1534
DNAPTFLGC.....G.C..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....	1540
MAJORITY	GCTCCACCAGCGCCCGTGCTGGAGGCCCTXCGXGAGGGCCCCACCCCATCGTGGAGAAGATCCTGCAGTA	
DNAPTAQC.....C..C.....	1604
DNAPTFLT.....G..A.....CCGC.....	1601
DNAPTTHG.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCXGXCCTCGTCCACCCCAAGACGGGC	
DNAPTAQG....G.....T.....G.A....A.....	1674
DNAPTFLA.....A.....C.C...G.....A...C...	1671
DNAPTTHG.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQA.....T.....C..	1744
DNAPTFLG.....C.....TCC.....	1741
DNAPTTHG.....G.....	1750

FIG. 2E

MAJORITY	AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCGGGCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQG..T..G.....A.C.....G...C.	1814
DNAPTFLG.....T.....C.C.....A.....C.....	1811
DNAPTTHCT.....C.....T.....C.....T.....C	1820
MAJORITY	GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....T.....T.....A...G.....C.....	1884
DNAPTFL	.C.....T.T.....C.....T.....T.....	1881
DNAPTTHC.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCCGCGCTGGATGTTCCGGCGTCCCCCCCCG	
DNAPTAQC.....C.....GG.....G.....G...	1954
DNAPTFLT.....T.....T.....T.....T.....C.	1951
DNAPTTH	...A.....A.....A.....A.....	1960
MAJORITY	AGGCCGTGGACCCCTGATGGCGCCGGGGCCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCCGGC	
DNAPTAQT.....T.....G.....G...	2024
DNAPTFL	.A.GG..A.....T.....G.....G.....	2021
DNAPTTHGG.G.....C.....	2030
MAJORITY	CCACCGCCTCTCCCAGGAGCTTGCCATCCCCCTACGAGGAGGGGTGGCCTTCATTGAGCGCTACTTCCAG	
DNAPTAQA.....T.....CCA.....T...	2094
DNAPTFLGG.....T.....T.....	2091
DNAPTTH	...TA.G.....T.A.....A	2100

FIG. 2F

MAJORITY	AGCTTCCCCAAGGTGCGGCGCTGGATTGAGAAAGACCCCTGGAGGAGGCGCAGGAGGGGGGTACGTGGGAGA	
DNAPTAQ	2164
DNAPTFL	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTHA.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTCGGCGCGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAGAGCGGTGCGGAGGCGGCGGA	
DNAPTAQC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....C.....	2231
DNAPTTH	...AA.AA.....CA.....C.....	2240
MAJORITY	GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCCGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQT.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGCCCC	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTHC..C.G...G.....C.C.....CC...G.....	2380
MAJORITY	CAAAGAGCGGCGGAGGXGGTGGCCGCTTTGGCCAAAGGAGGTCAATGGAGGGGGTCTATCCCTGGCCGT	
DNAPTAQA.....CC.....CGGC.....G.....	2444
DNAPTFL	...G..C.....AG...A.....GG.....CAG..	2441
DNAPTTH	...C...C.....C.....A.....C.....C.....	2450

FIG. 2G

FOOT" 992860

MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQA.....GA	2499
DNAPTFLCC.....	2496
DNAPTTHT.....GT...	2505

FIG. 2H

MAJORITY	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFSAKLLKALKEDG·DAVXVVVFDK	
TAD PRO	.RG.....H.....I.....	69
TFL PROV.V.....	68
TTH PRO	.E.....YK..F.....	70
MAJORITY	APSRHEAYEAYKAGRPTPEFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL	
TAG PROGG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDNLPGVKGIGEXTAKLLX	
TAG PROK.....H.....D.A.....T.E.....R...E	209
TFL PROE...I.....Y.....A.....I.....QR..IR	208
TTH PROV...V.....H...E.....F...V.....L...K	210
MAJORITY	EWGSLNLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLEF	
TAG PROA.....L...AI...L...D...K..WD.AK.....K.....R.....	278
TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PROENV...K..L...R..LE..R.....L.QG.....	280
MAJORITY	GSLLEHGLLEXPKALEEAPWPPPEGAFVGVLSRPEPMWAEALLAARXGRVHRAXDPLXGLRDLKEV	
TAG PROS.....K.....D.....PE.YKA.....A	348
TFL PROG..A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PROA.AP.....K.....C.D.....A...A..K.....	350

FIG. 3A

MAJORITY	RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGWETEDAGERALLSERLFXNLXX	
TAQ PROS.....G.P.....E.....A.....A..WG	418
TFL PRO	..I.....F.E.....A.....QT.KE	417
TTH PROS.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVFRLAGHPFNLNSRD	
TAQ PROR...R...A.....R.....A..A.....	488
TFL PRO	..K.....E.....R.....EA.V.Q.....	487
TTH PROK.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRTG	
TAQ PROR...L...Q.....R.....S.....D.I.....	558
TFL PRODR.....A...K..	557
TTH PROH.....V...S.....	560
MAJORITY	RLHTRFNQTATATGRLSSDPNLQNIPVRTPLGQRIIRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PROI.....L.....	628
TFL PROV..V.....	627
TTH PROA..A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPIYEEAVAFIERYFQ	
TAQ PROE.....R.....Q.....	698
TFL PROS..G.....G..S.....	697
TTH PROK.....V.....	700

FIG. 3B

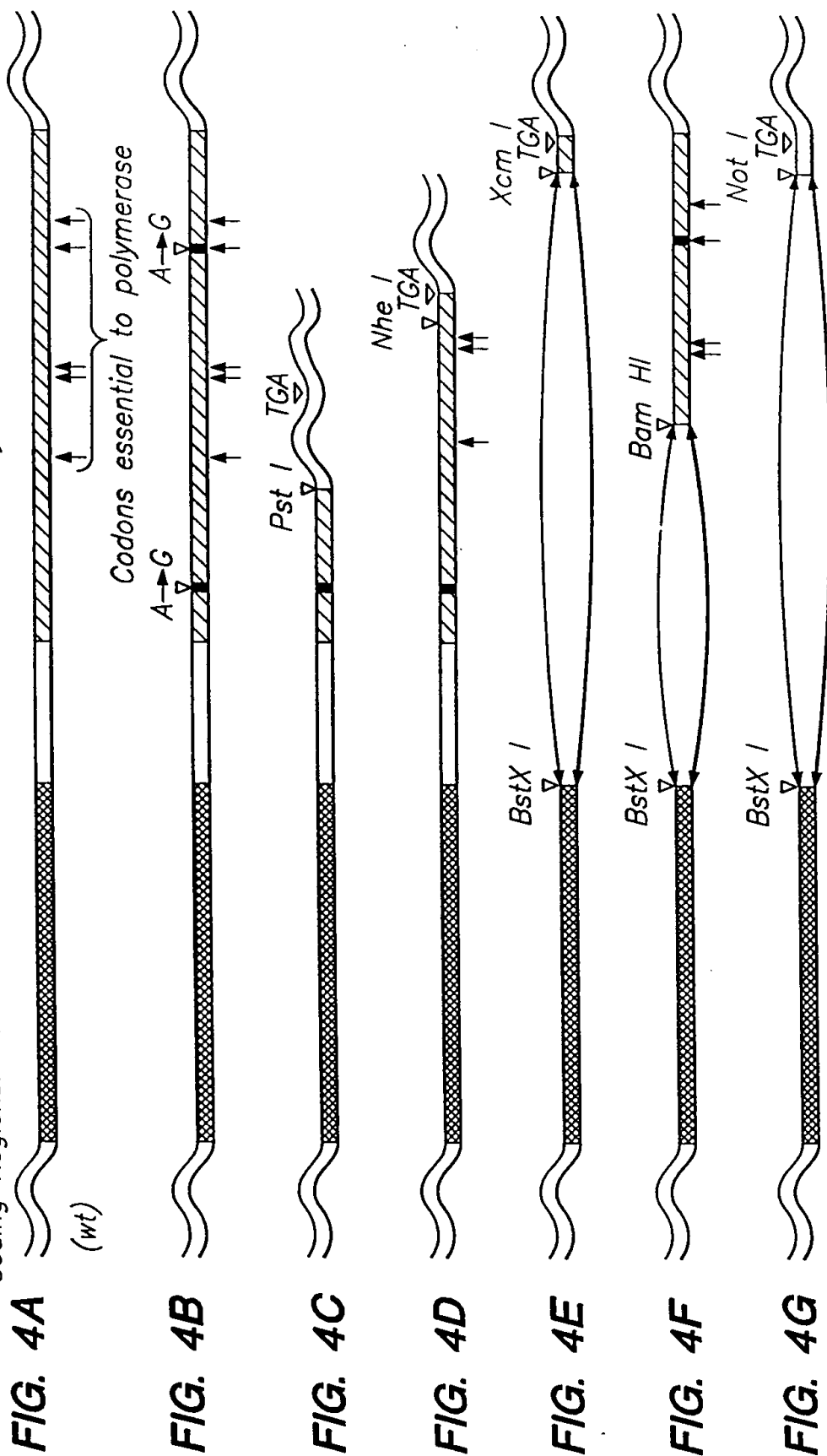
MAJORITY	SFPKVRWIEKTLEEGRRRGYVETLFGRRRYVPDLNARVKSVREAAERMAFNPVQGTAAADLMKLAMVKL	
TAQ PROE.....	768
TFL PRO	.Y.....G.....R.	767
TTH PROK.....	770
MAJORITY	FPRLXEMGARMLLQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PROE.....A..R.....I.....	833
TFL PROQ..L.....D...R.....W..Q.....L.....	831
TTH PROR.....L.....QA...E.....A..KA.....M.....G	835

FIG. 3C

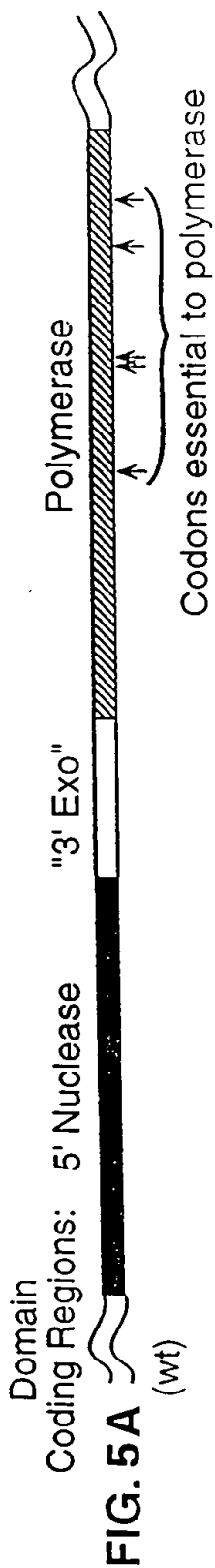
Genes for Wild-Type and Pol(-)DNAPTaq

Domain
Coding Regions: 5' Nuclease

Polymerase



Genes for Wild-Type and Pol(-)DNAPTfl



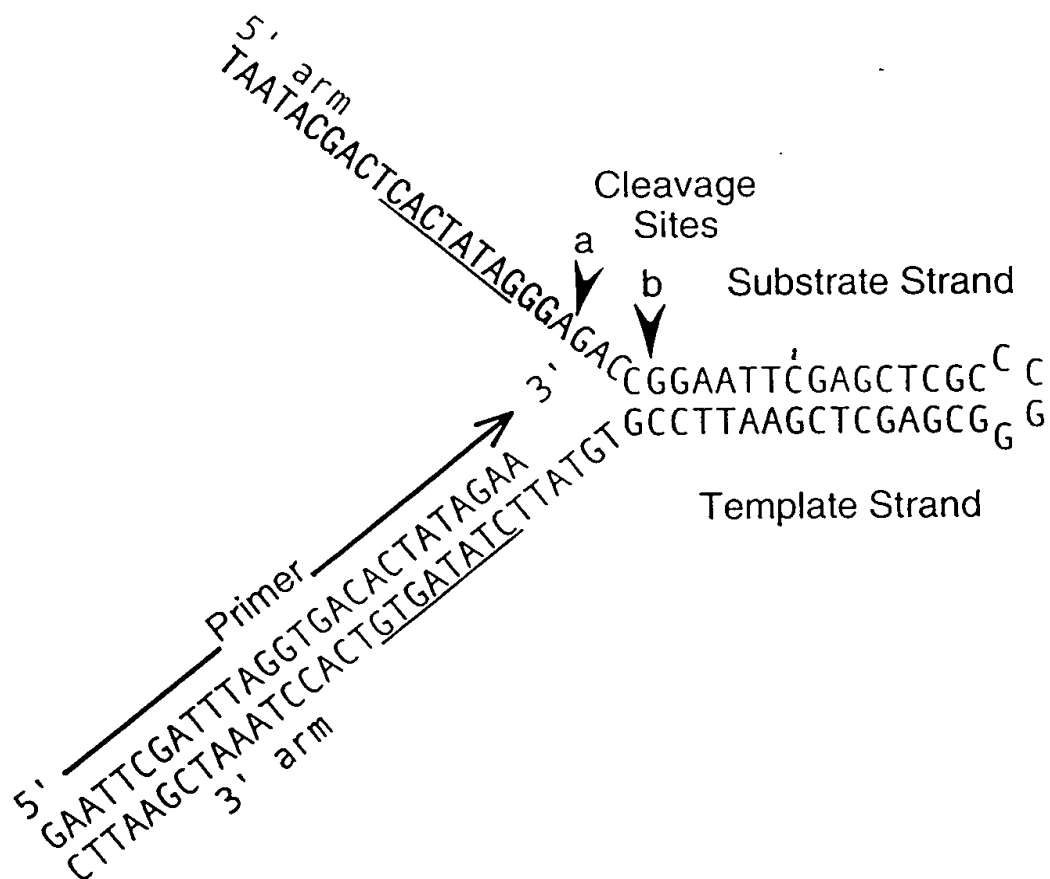


FIG. 6

09982667-101801

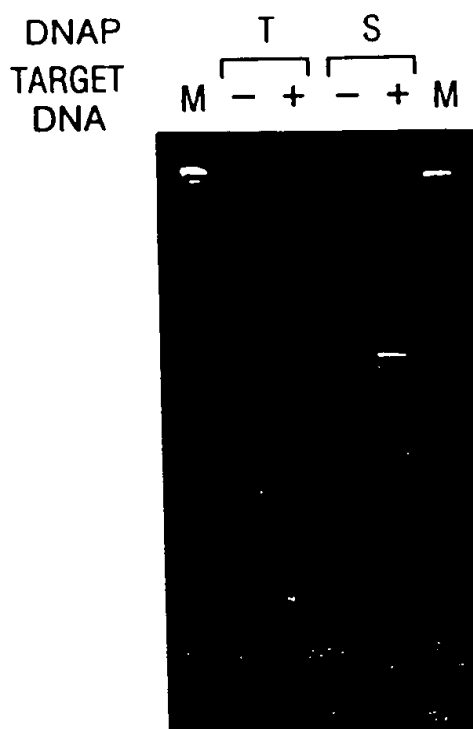


FIG. 7

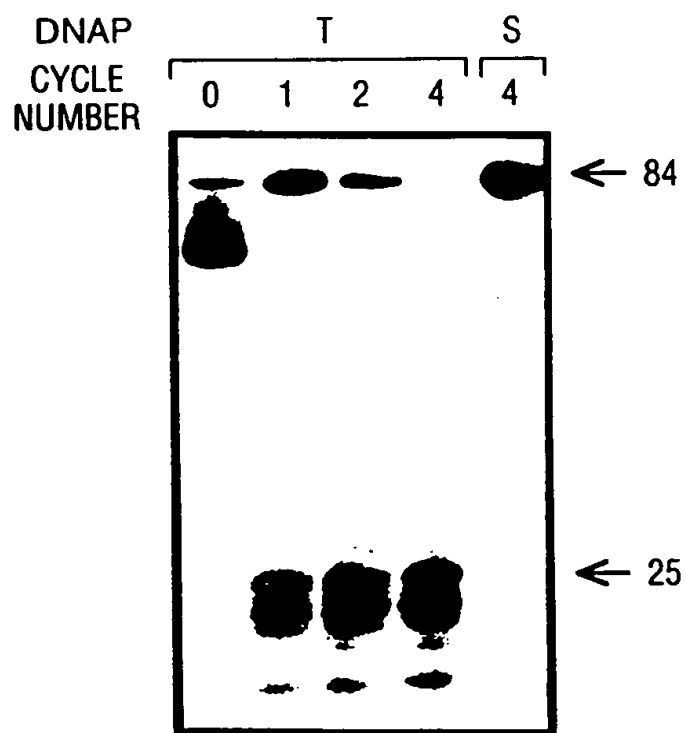


FIG. 8

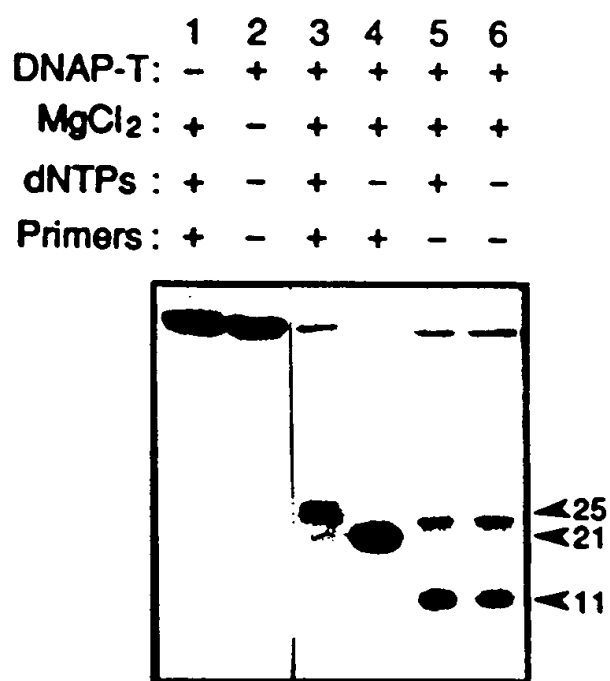


FIG. 9A

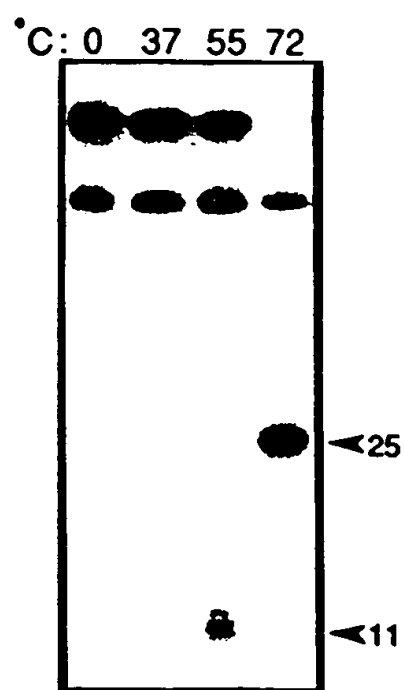


FIG. 9B

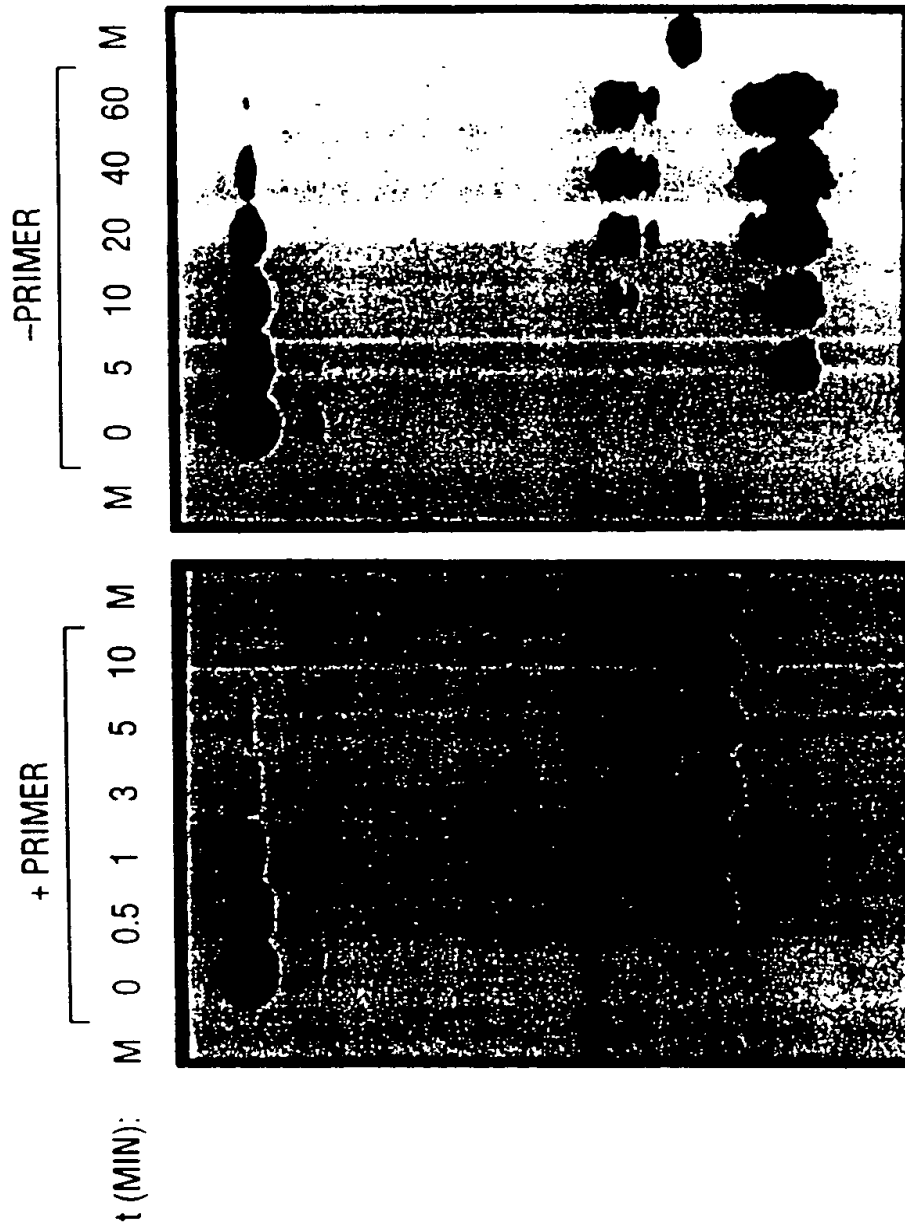


FIG. 10B

FIG. 10A

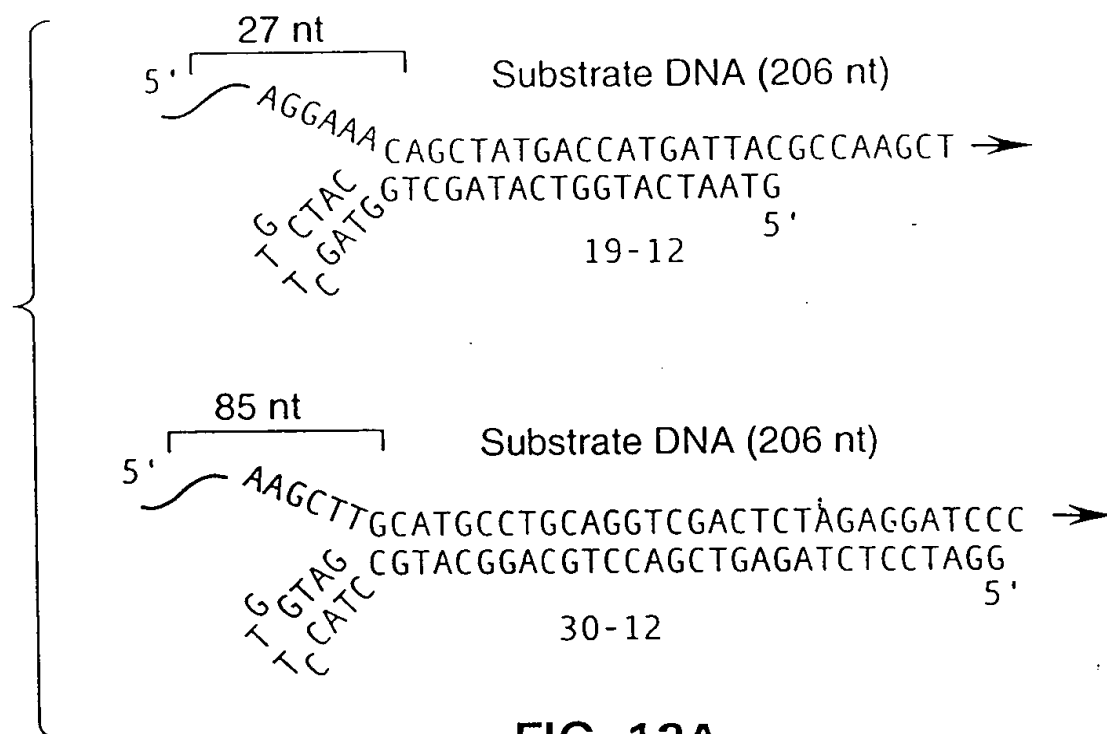


FIG. 12A

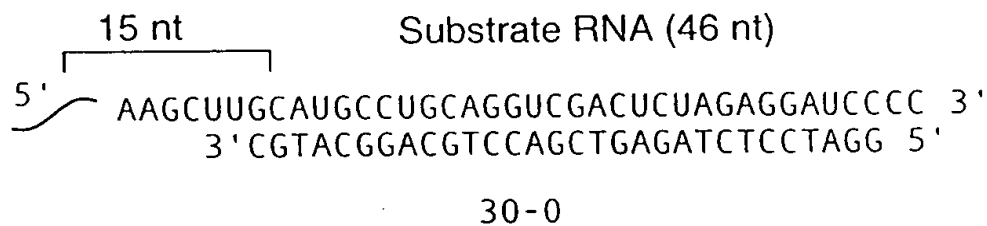


FIG. 13A

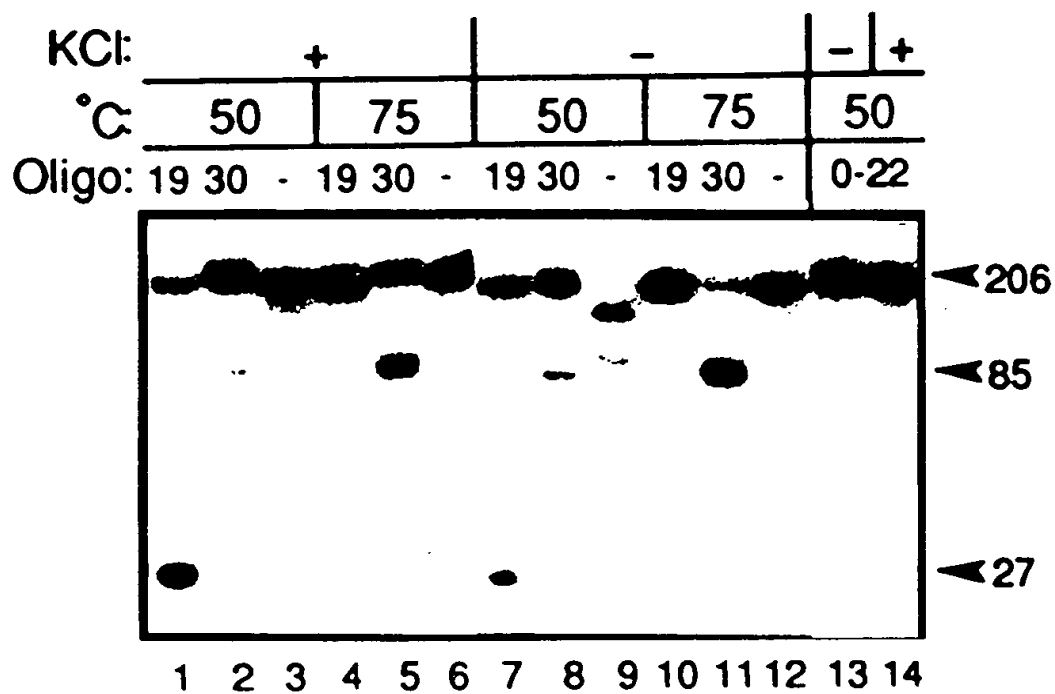


FIG. 12B

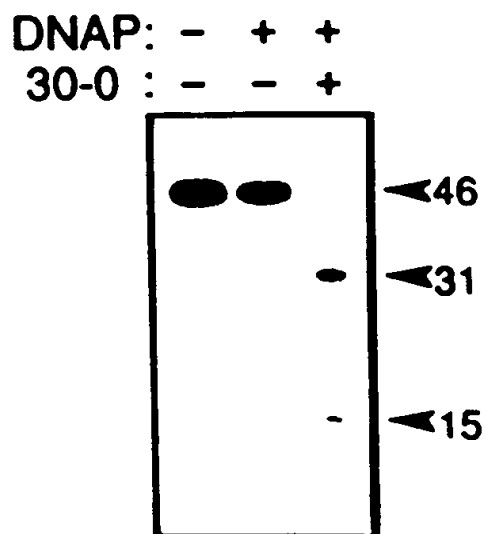
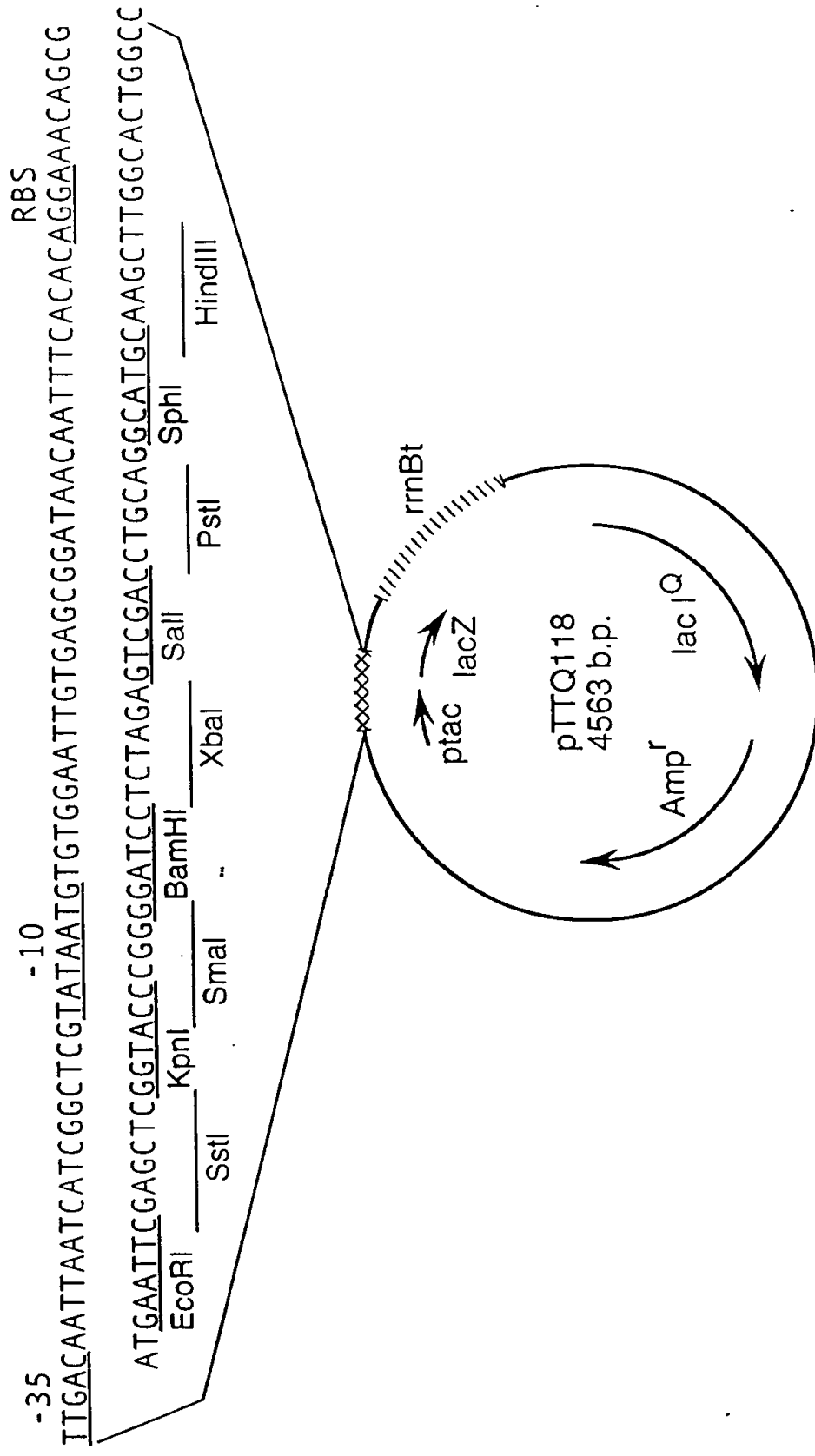


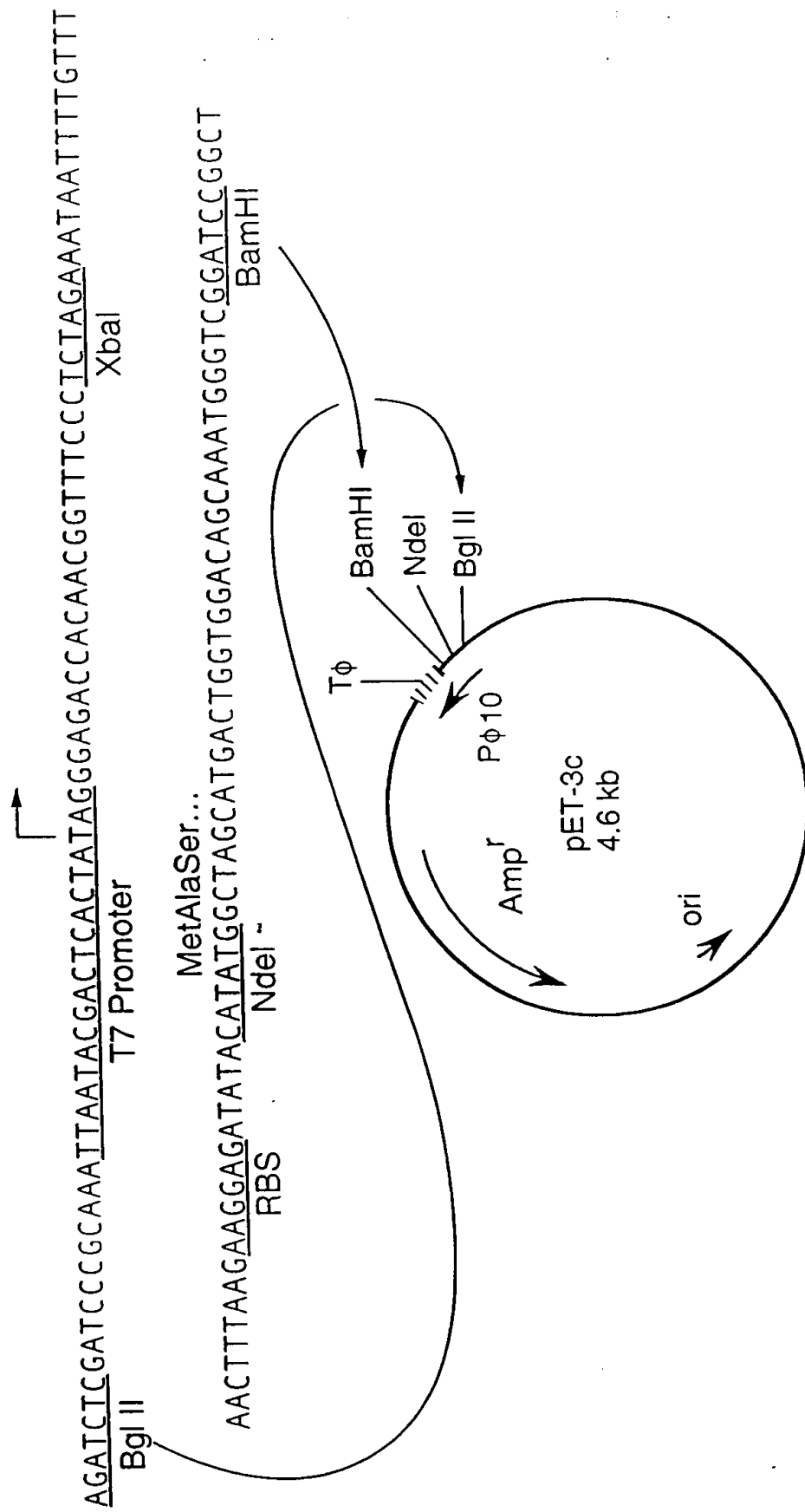
FIG. 13B



RBS: Ribosome binding site
 lacZ: Beta-galactosidase alpha fragment
 ptac: Synthetic tac promoter
 lac I^Q: Lac repressor gene
 rrnBt: E. coli rrnB transcription terminator

FIG. 14

TCBCT" 2928660



P_{φ10}: Bacteriophage T7 $\phi 10$ promoter RBS: Ribosome binding site
T_φ: T7 ϕ Terminator

FIG. 15

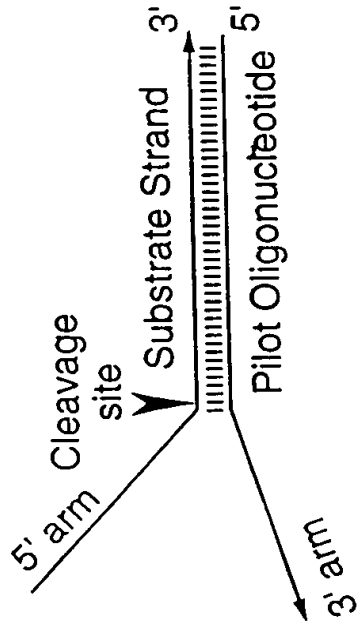


FIG. 16A

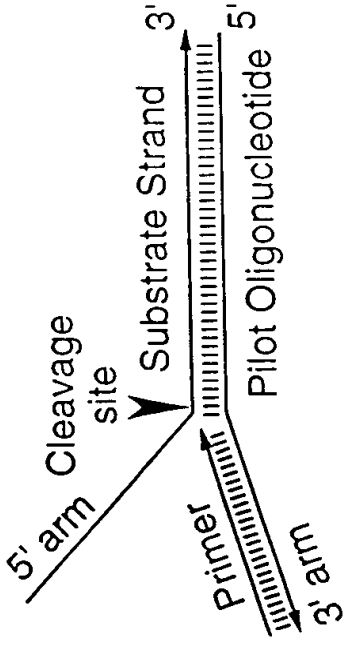


FIG. 16B

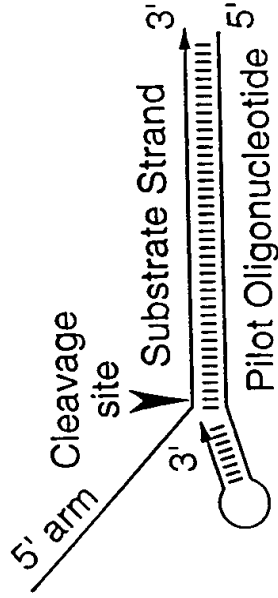


FIG. 16C

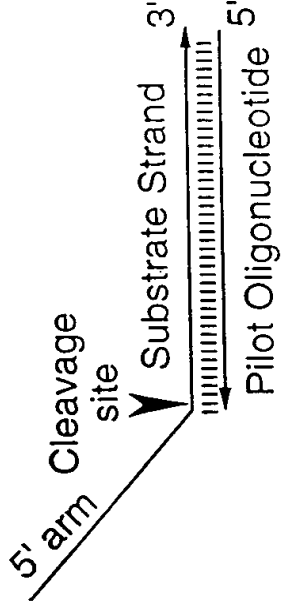


FIG. 16D

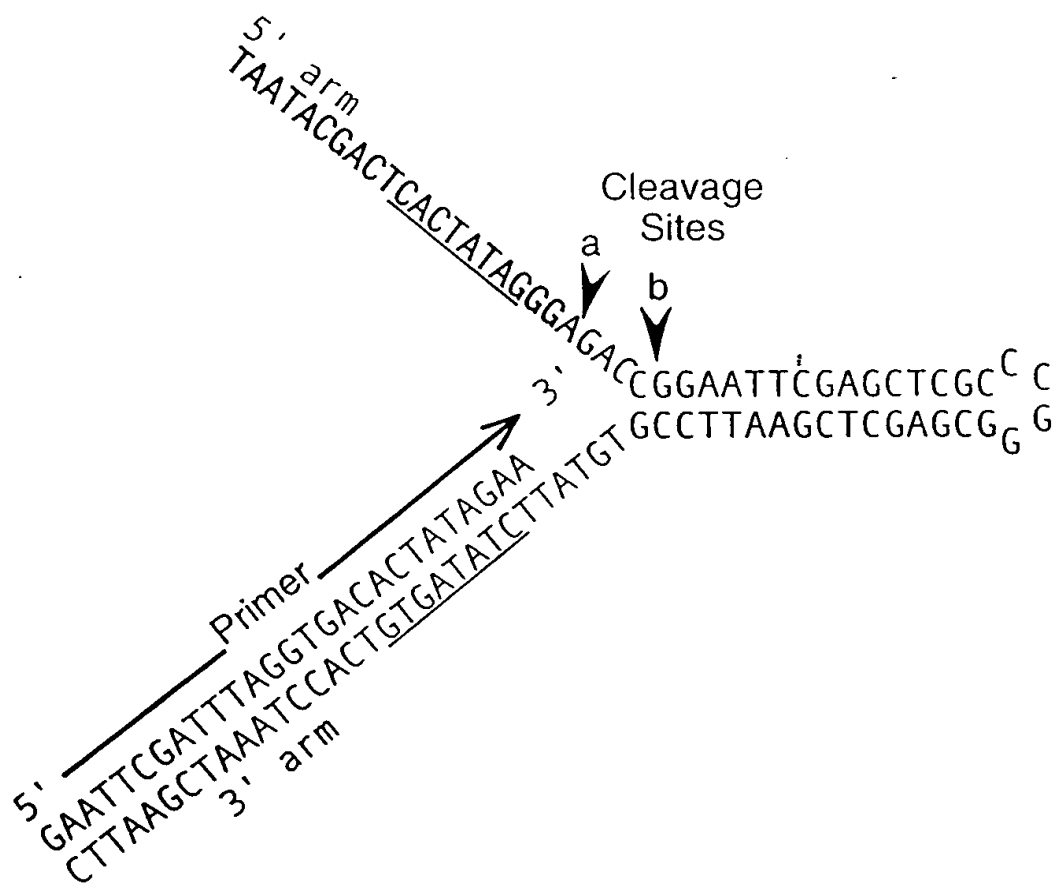


FIG. 16E

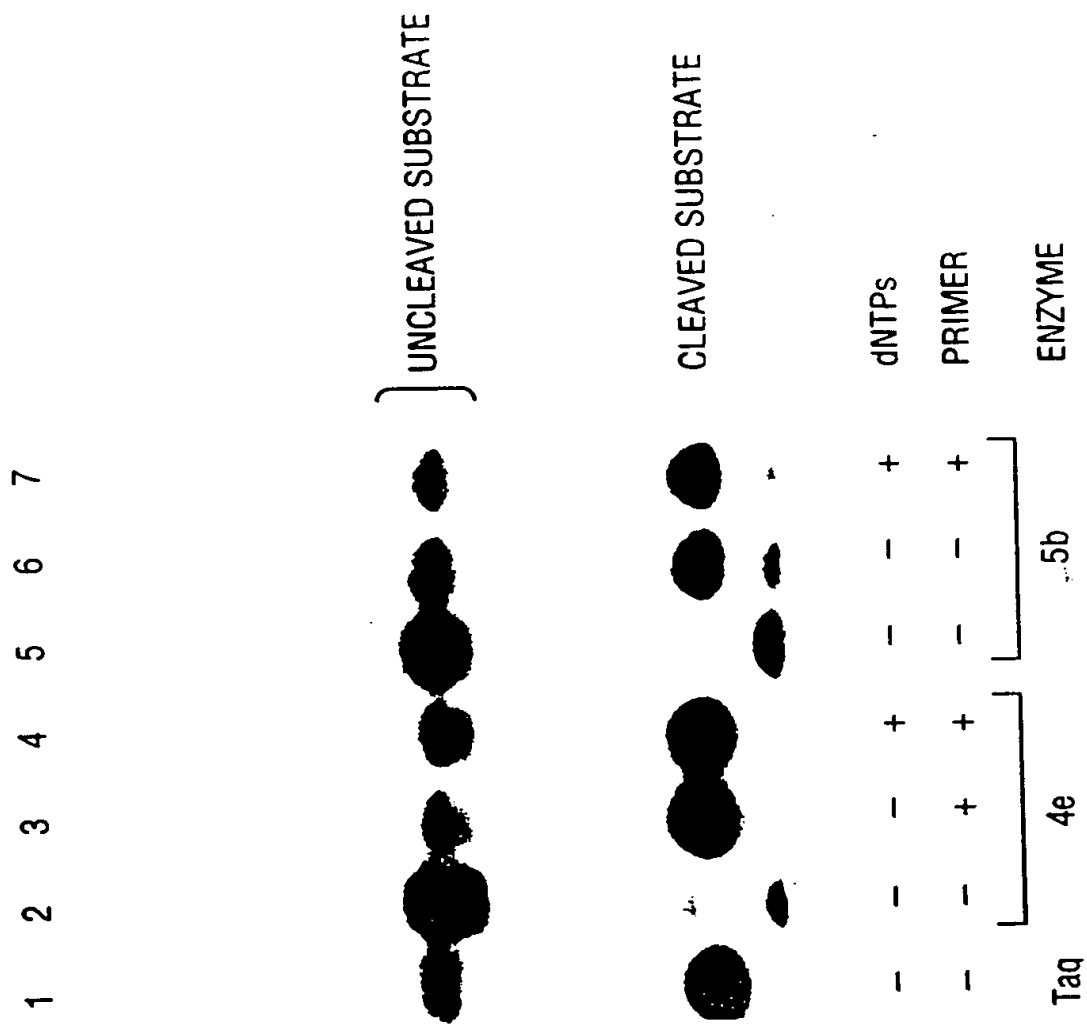


FIG. 17

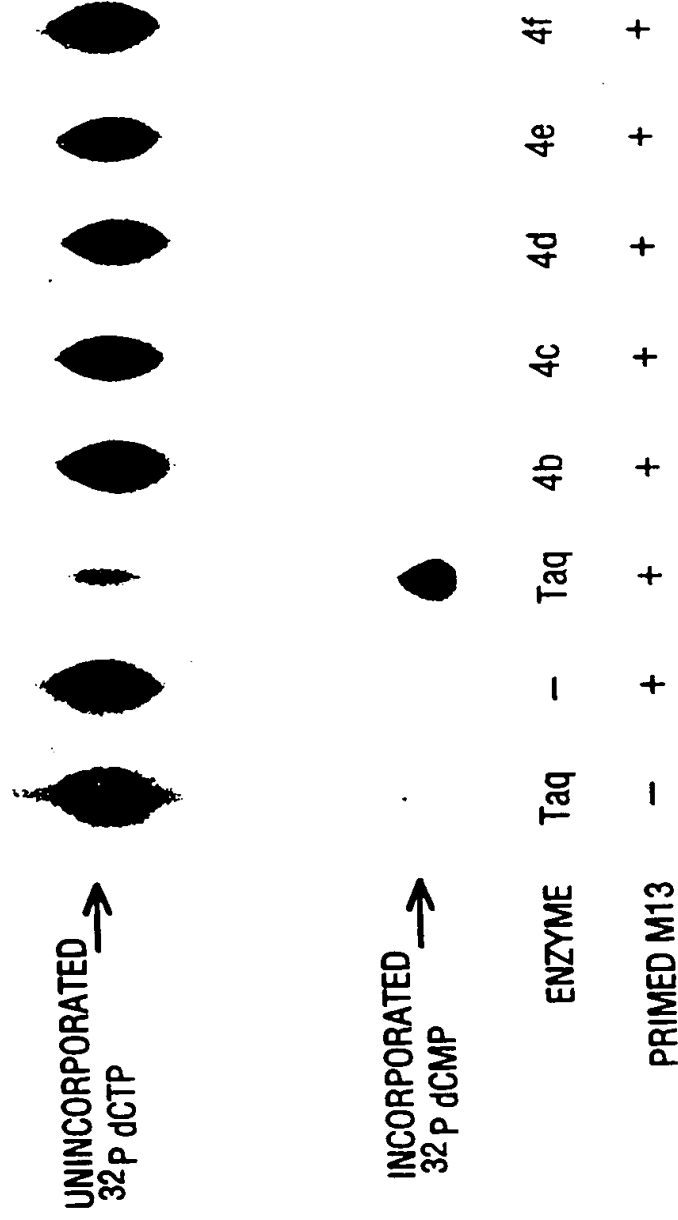


FIG. 18

(32p) 5' TAATACGACTCACTATAGGGAGACCGGAAT T C
SITES OF CLEAVAGE WITH A GAP OF 6 nt.
60% Y 40%
5' GATTTAGGTGACACTATAG 3' A G
CTTAAGCTAAATCCACTGTGATATCTTATGTGCCTTA A G
3'

FIG. 19A

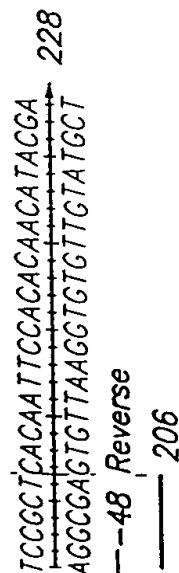
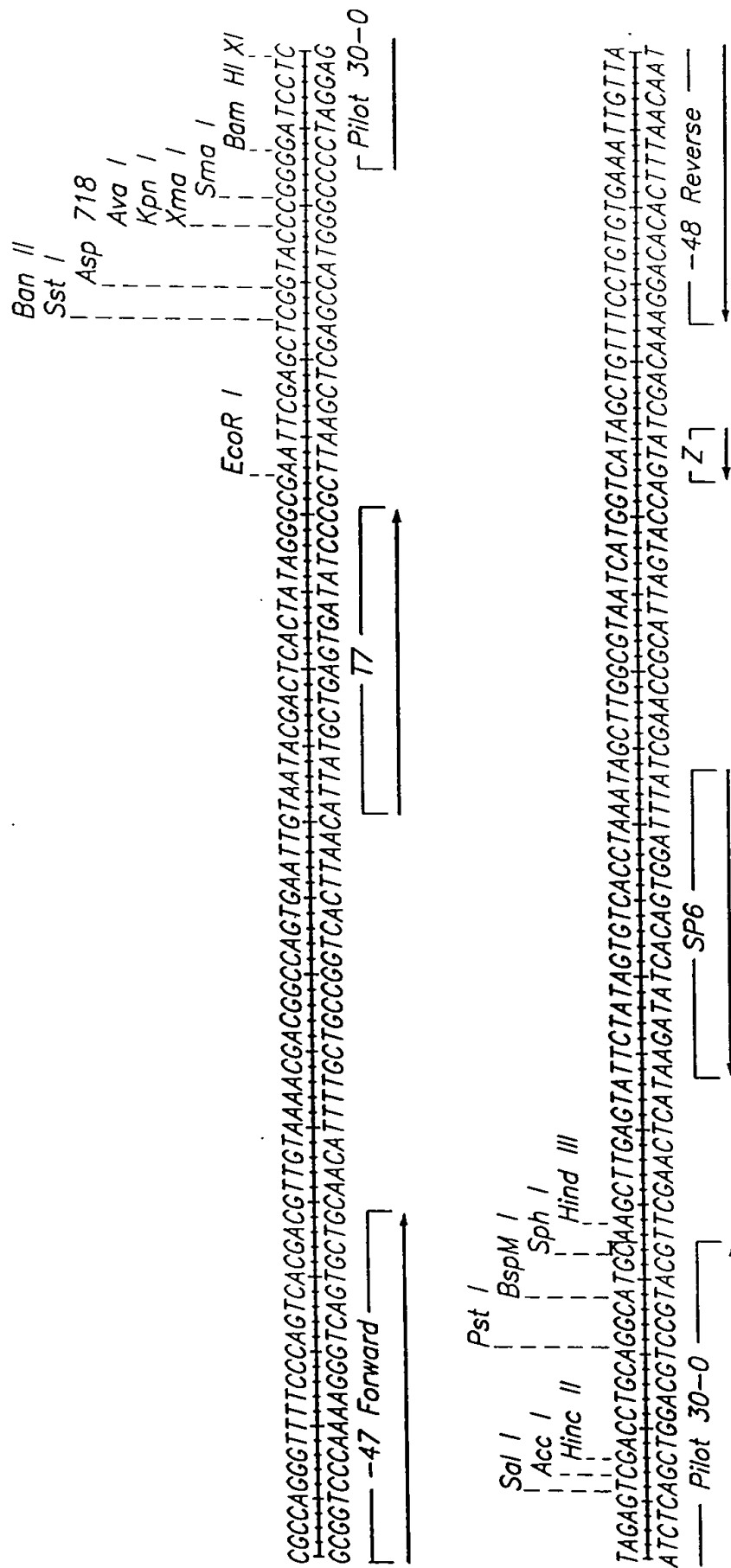


FIG. 21

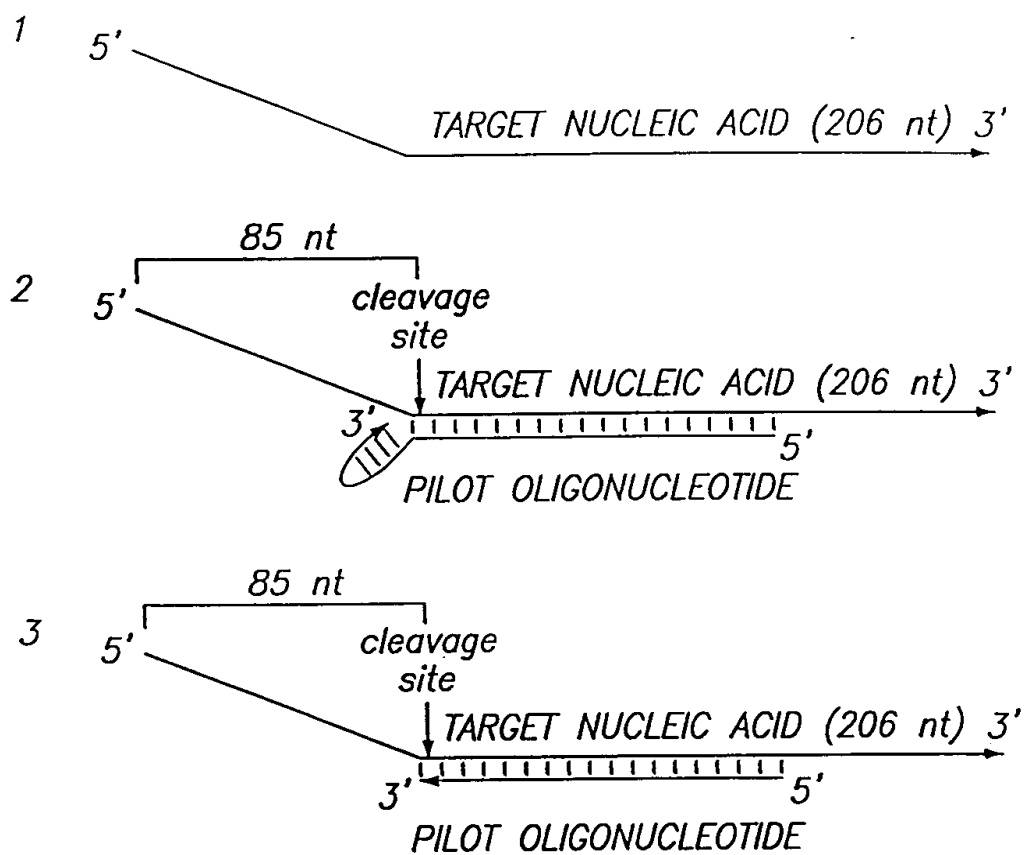


FIG. 22A

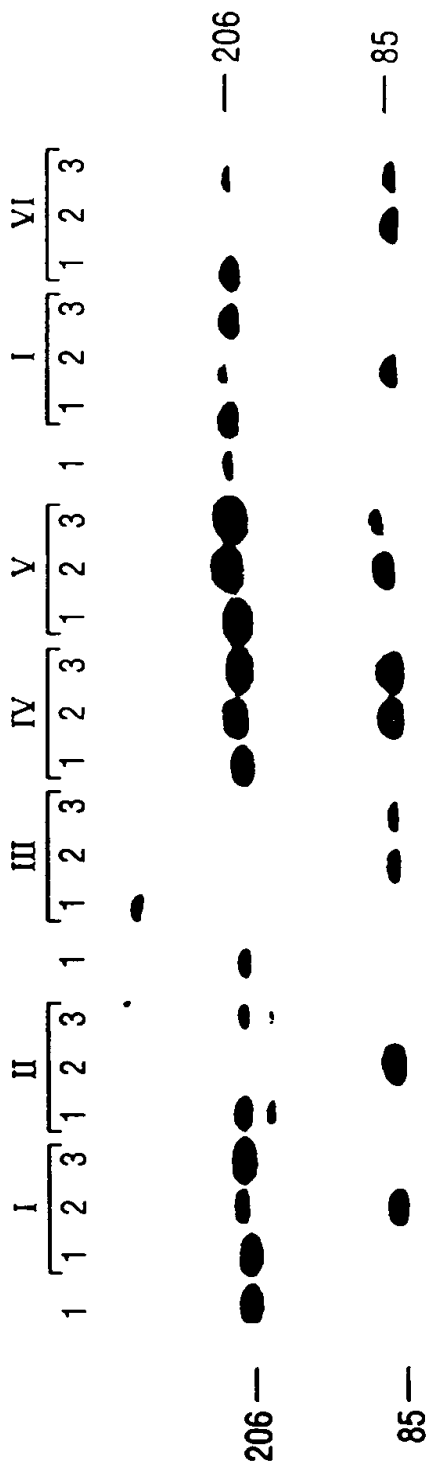


FIG. 22B

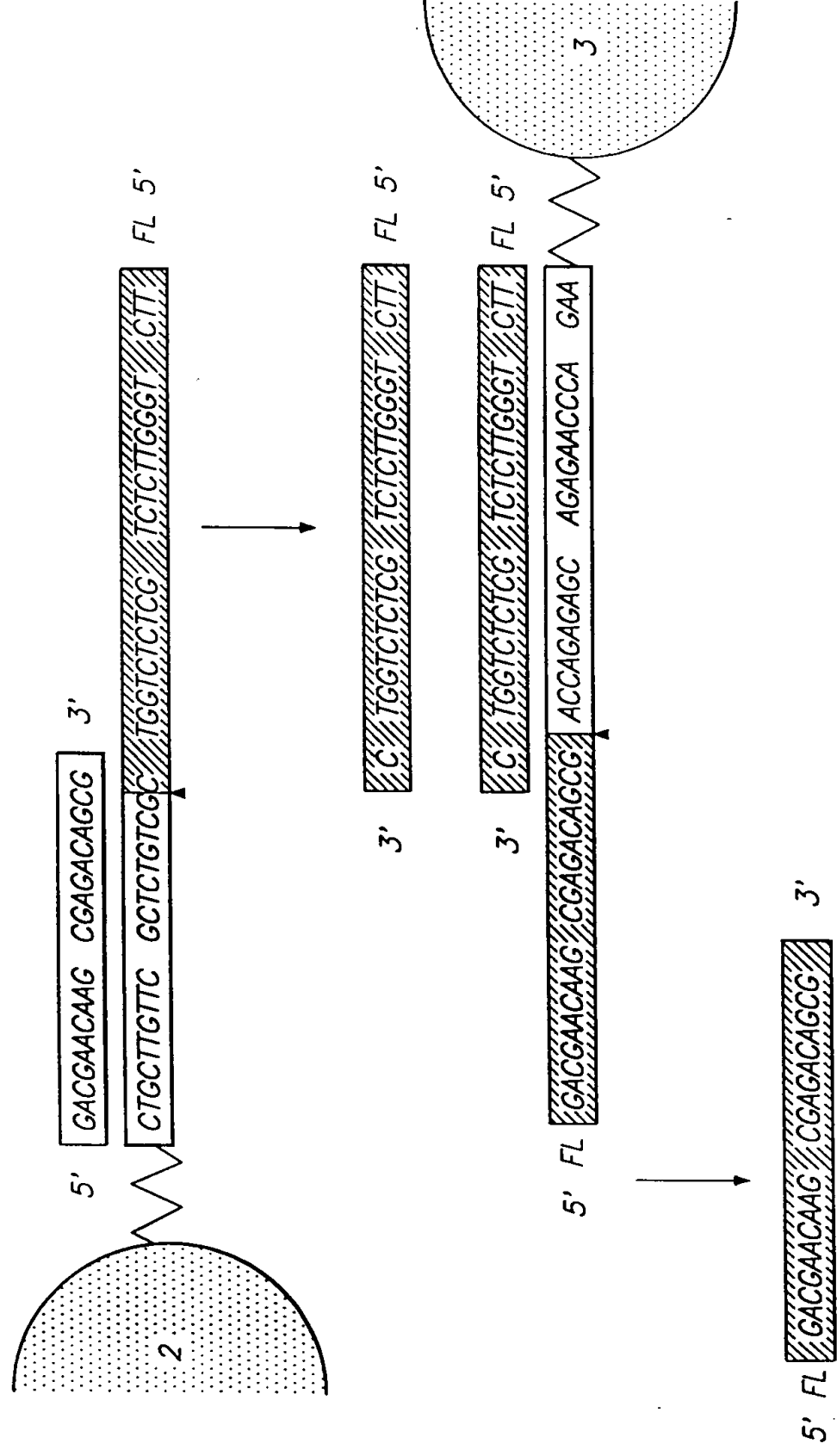


FIG. 23

FOBTOT 29928660

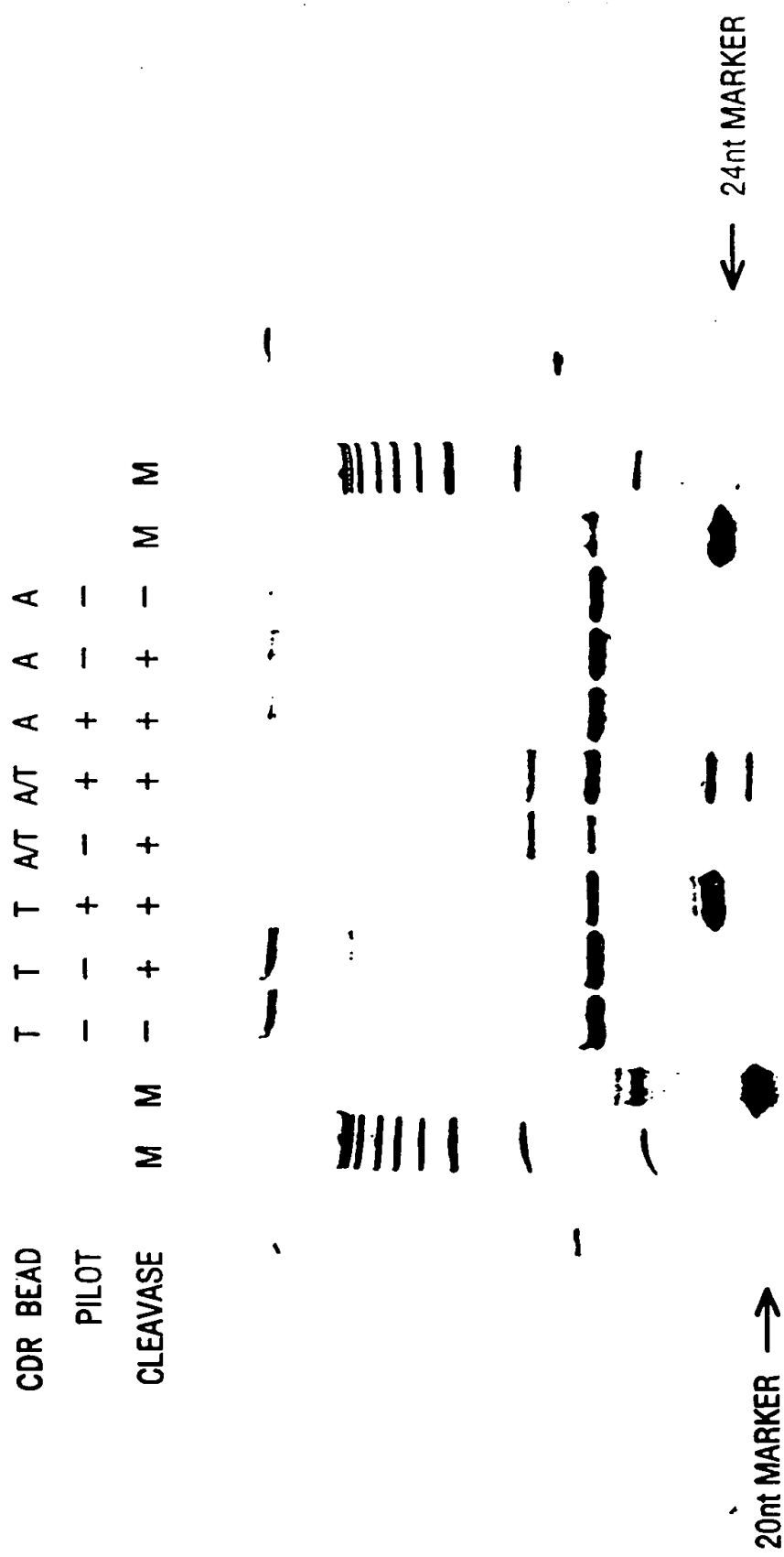


FIG. 24

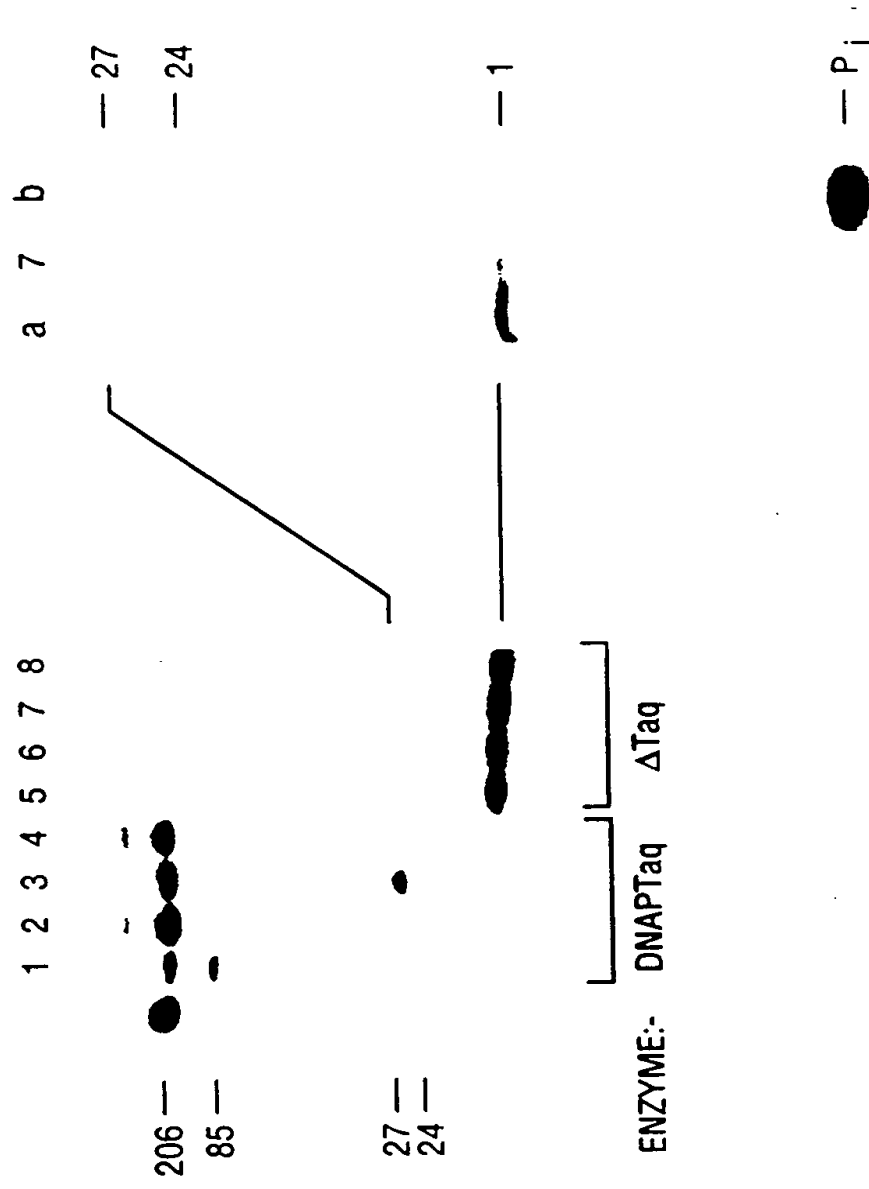


FIG. 25A

FIG. 25B

FIG. 26A

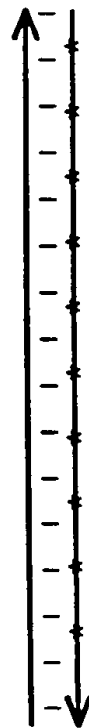


FIG. 26B

* = 32p



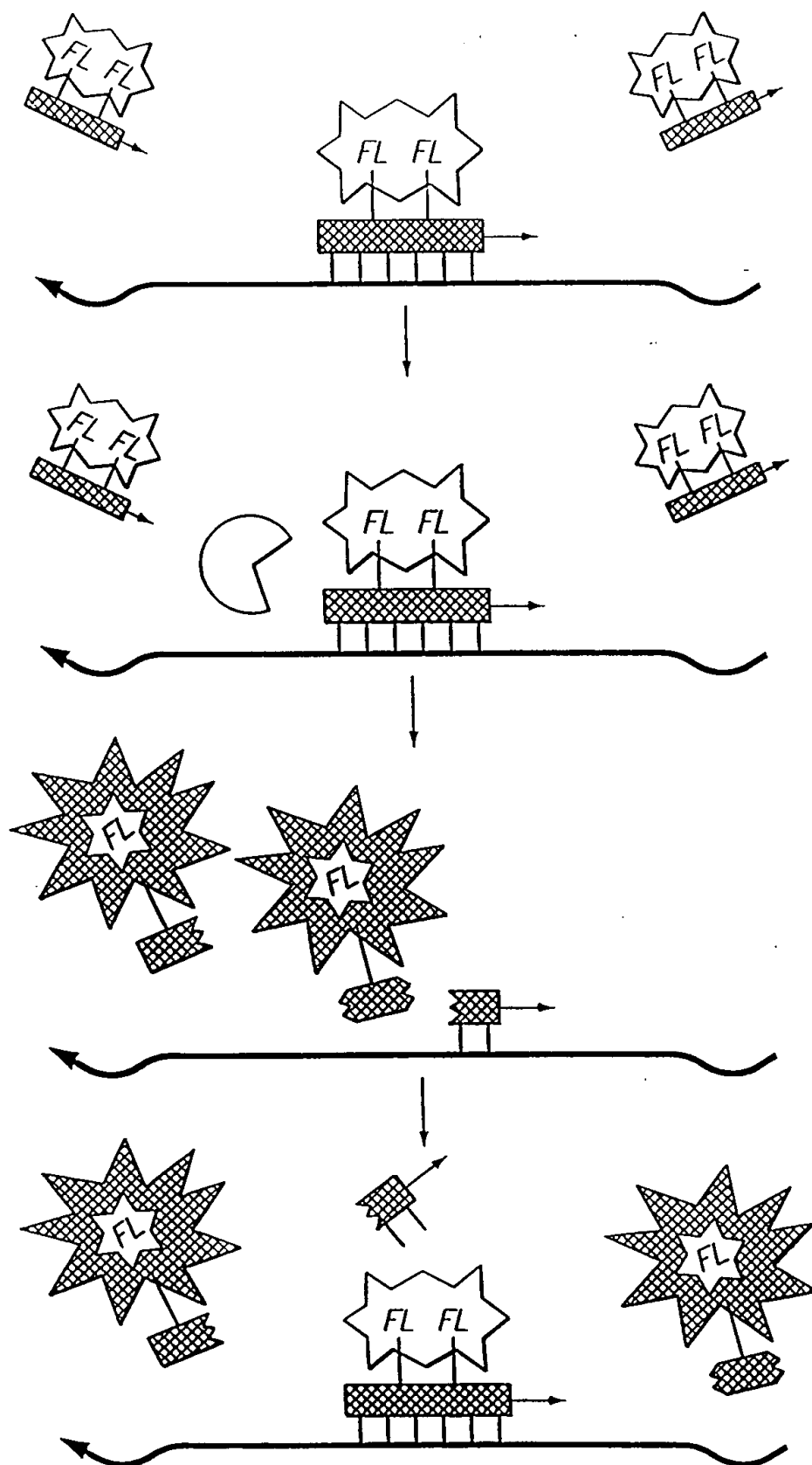


FIG. 27

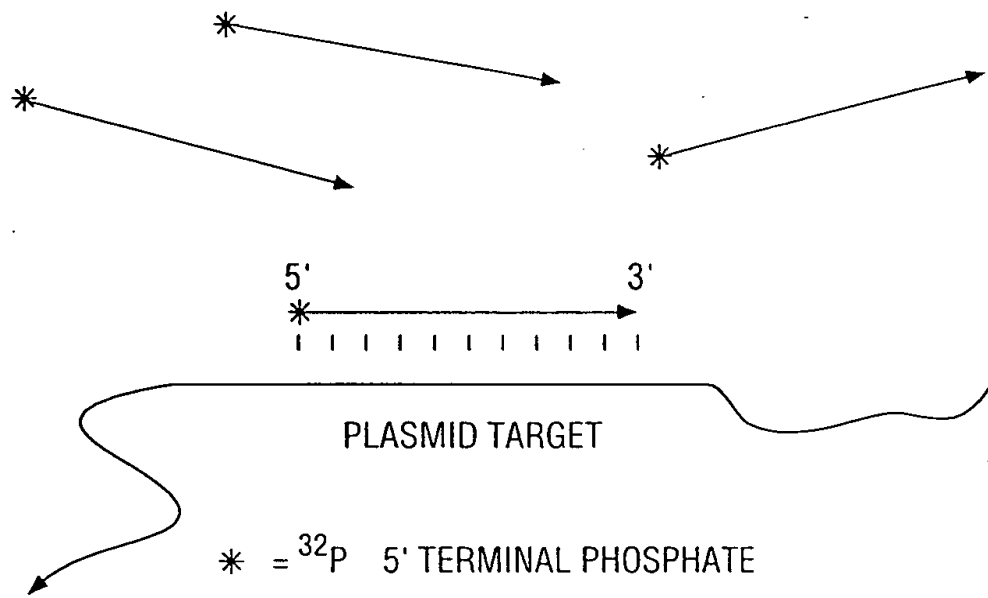


FIG. 28A

09982667-101801

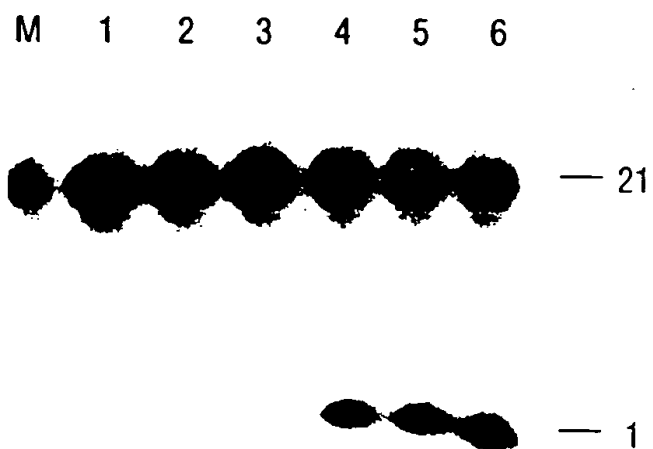


FIG. 28B

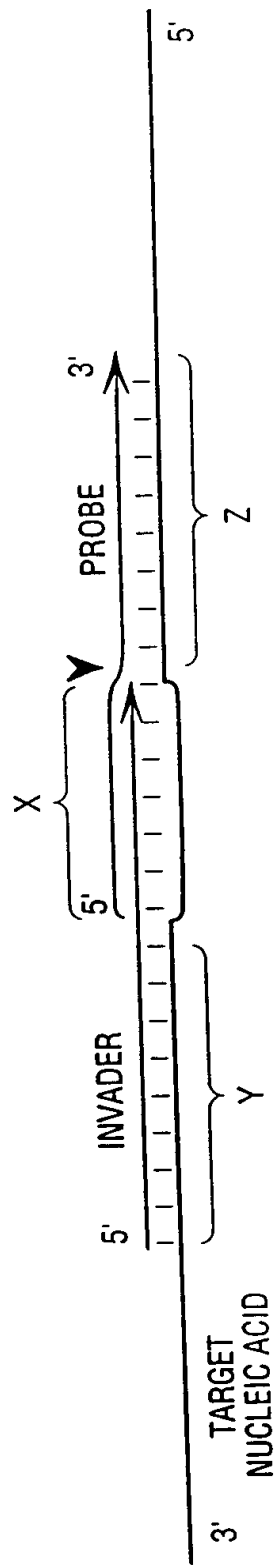


FIG. 29

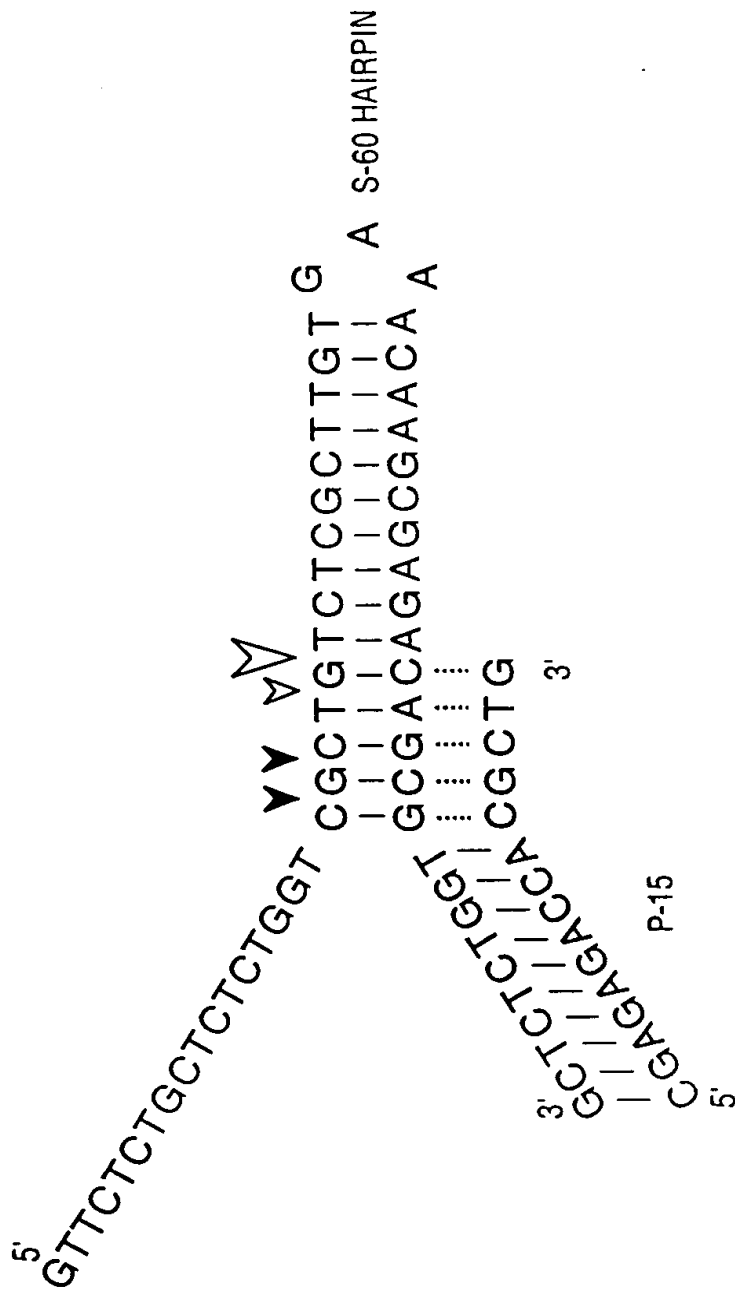


FIG. 30

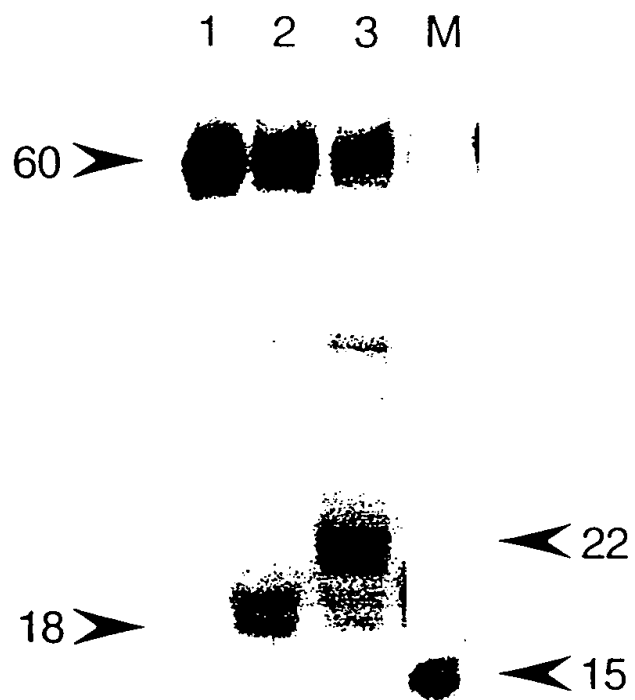


FIG. 31

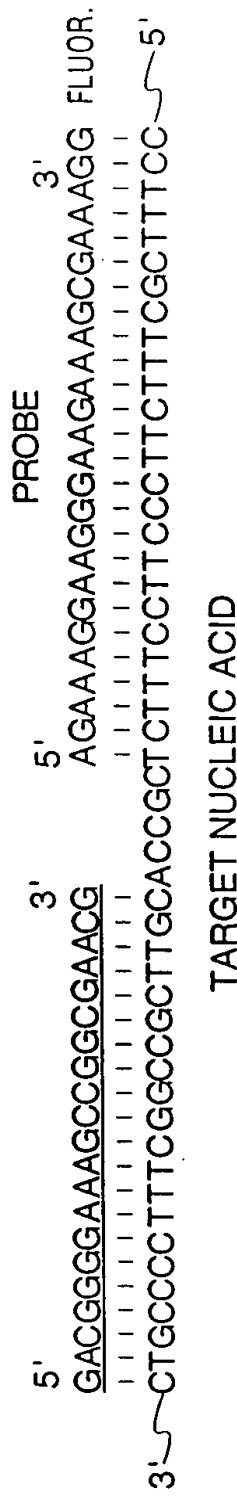


FIG. 32A

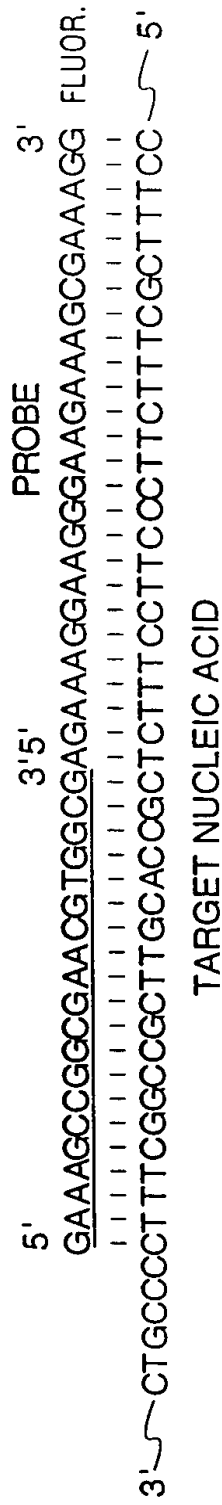


FIG. 32B

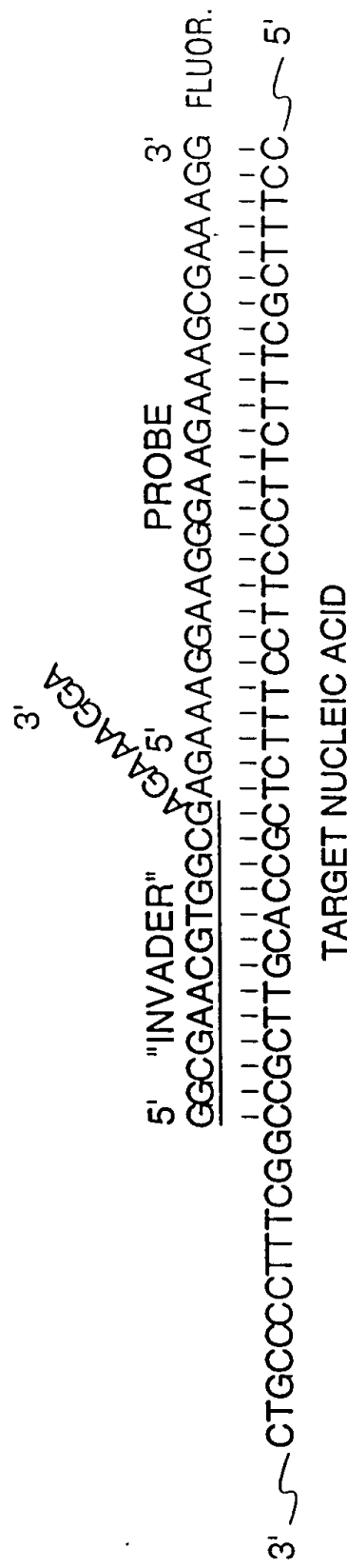
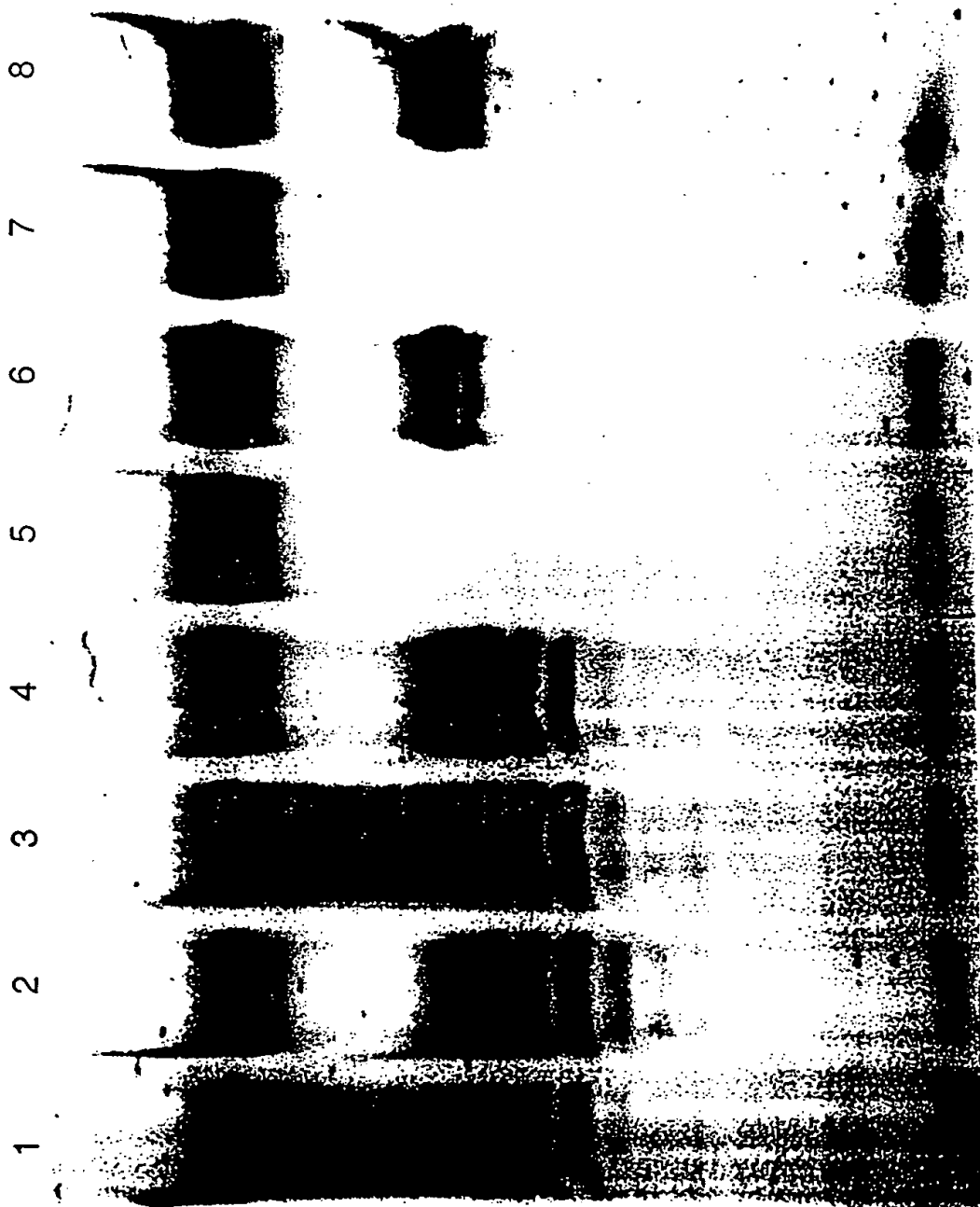


FIG. 32C

FOOTOT 29928660



26

FIG. 33

FOROT 2928660

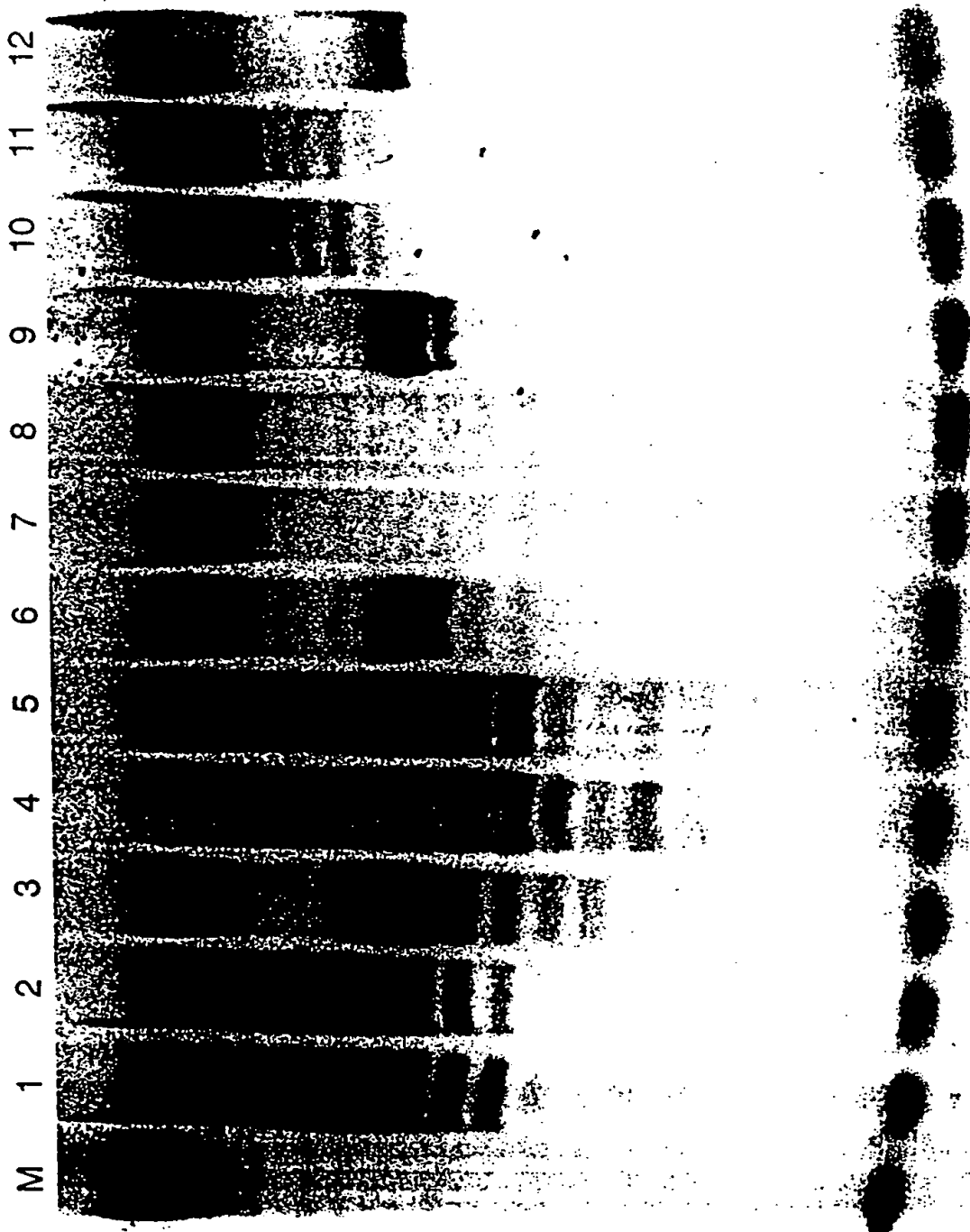


FIG. 34

09982667-101801

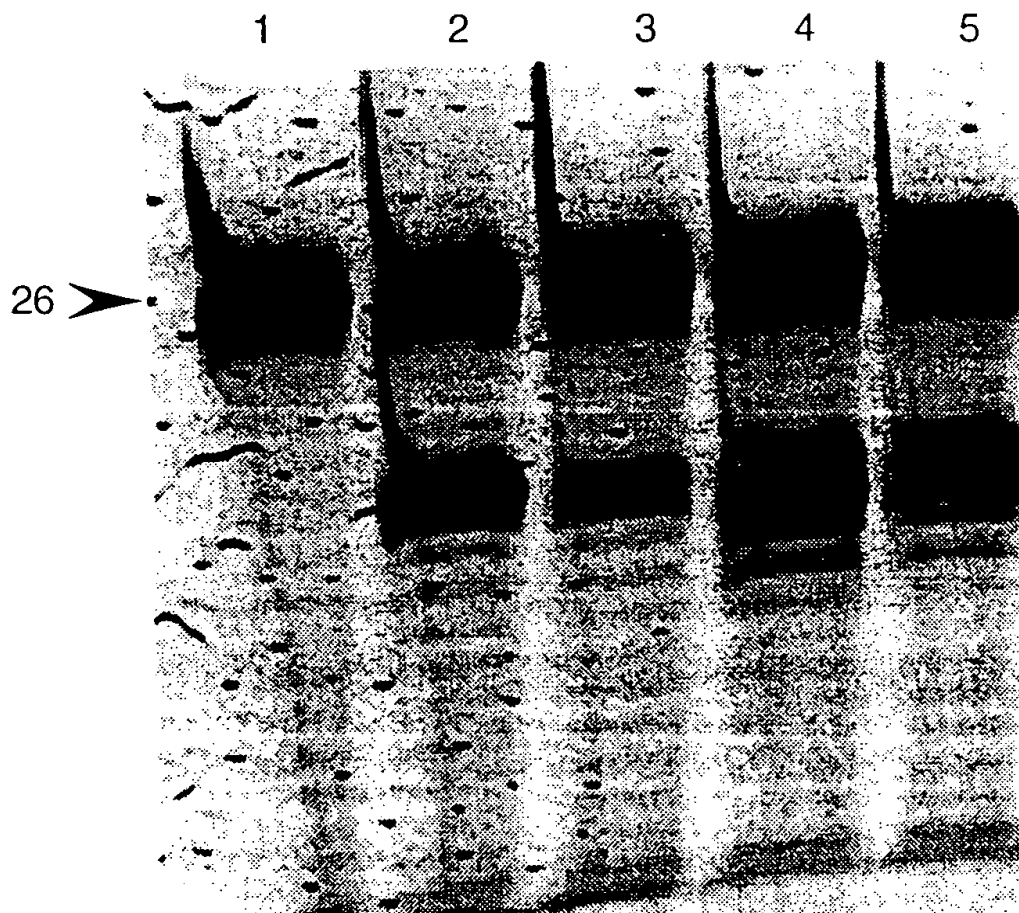


FIG. 35

TOPOT 29928660

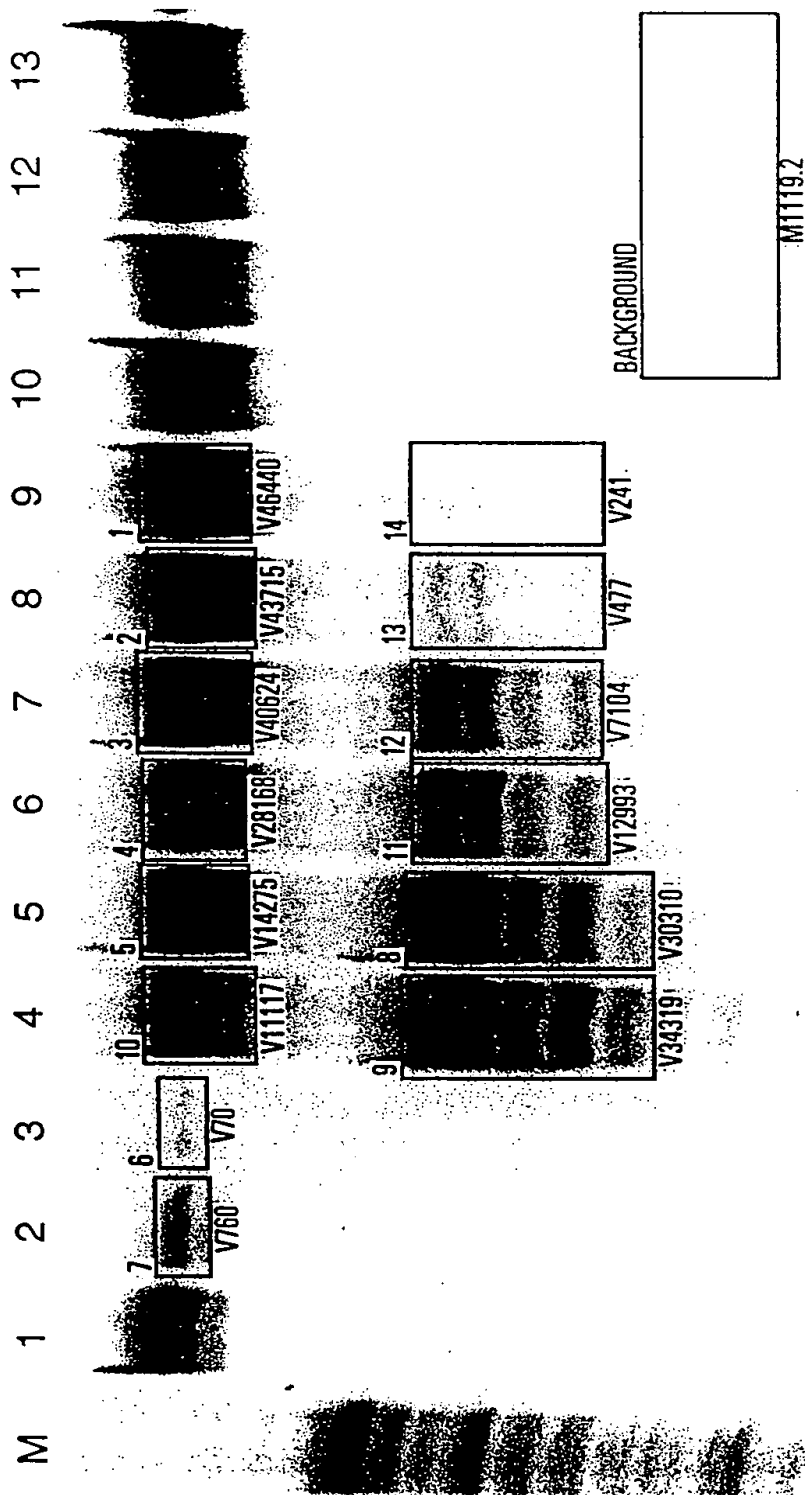


FIG. 36

FOSTOT 29928660

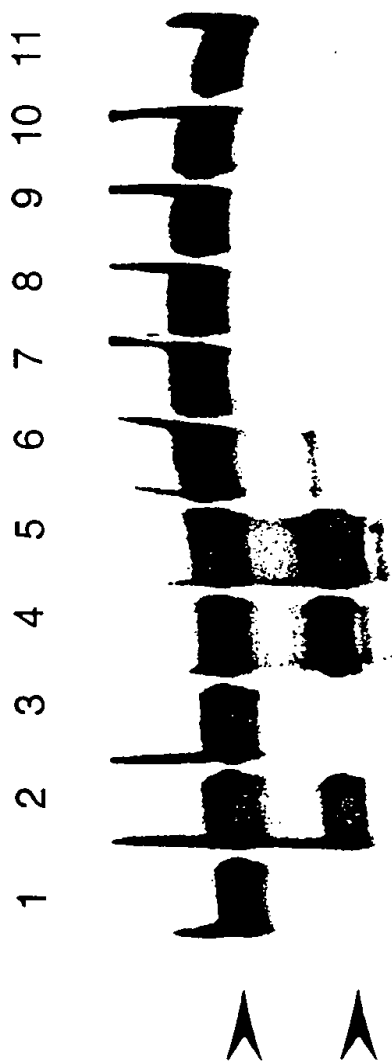


FIG. 37

FOOT" 292860

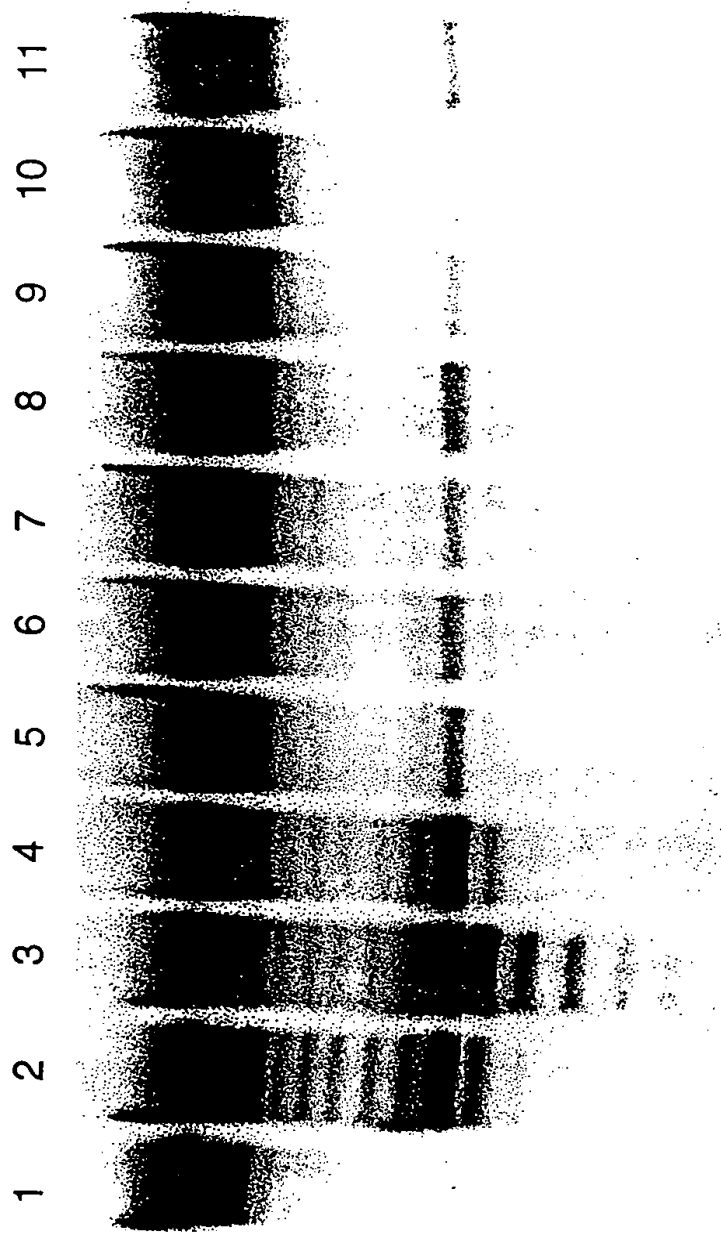


FIG. 38

09982657-101801



FIG. 39

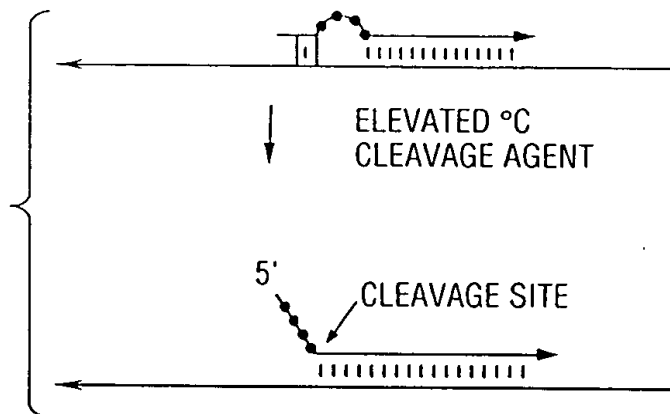


FIG. 40A

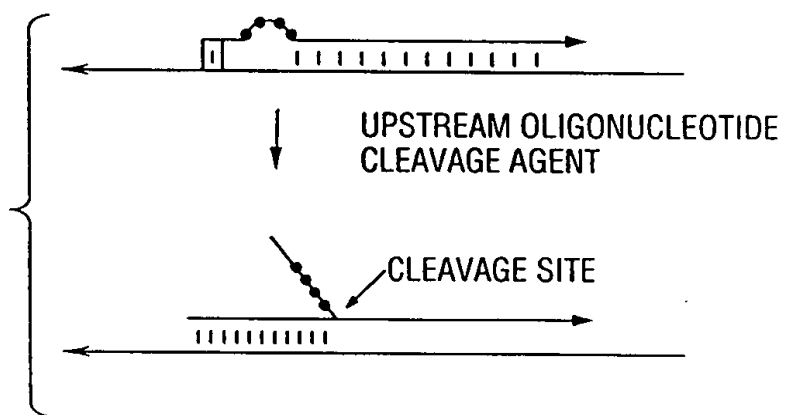


FIG. 40B

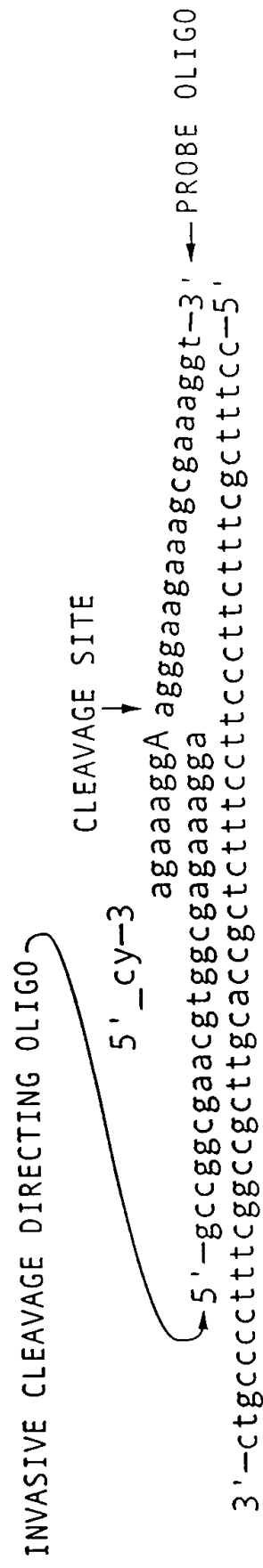


FIG. 41

09982667-101801

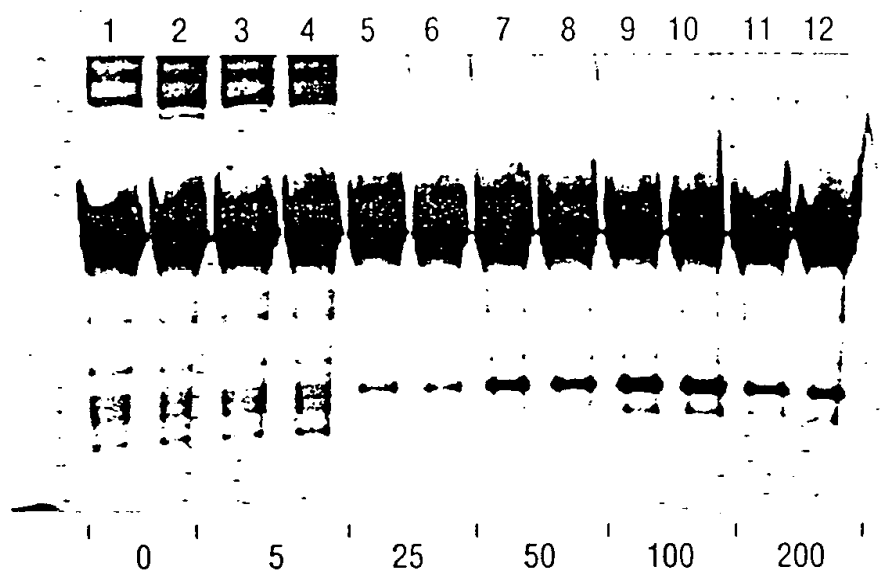


FIG. 42

09982667-101801

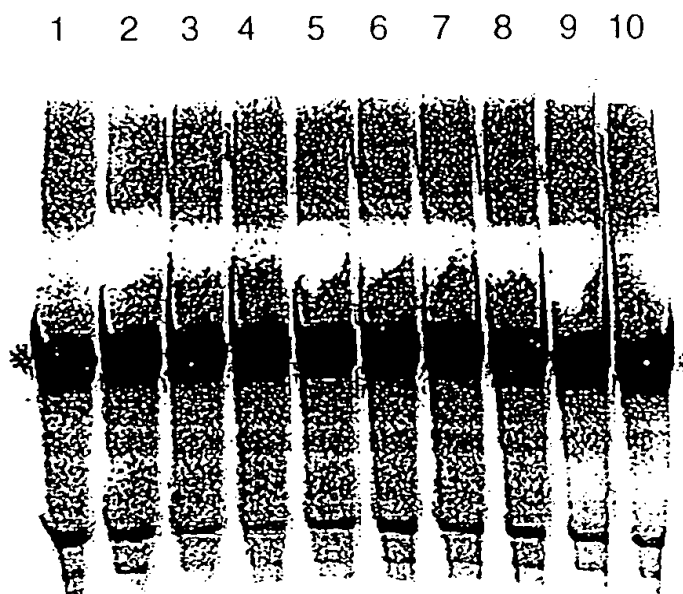


FIG. 43

09982667-101801

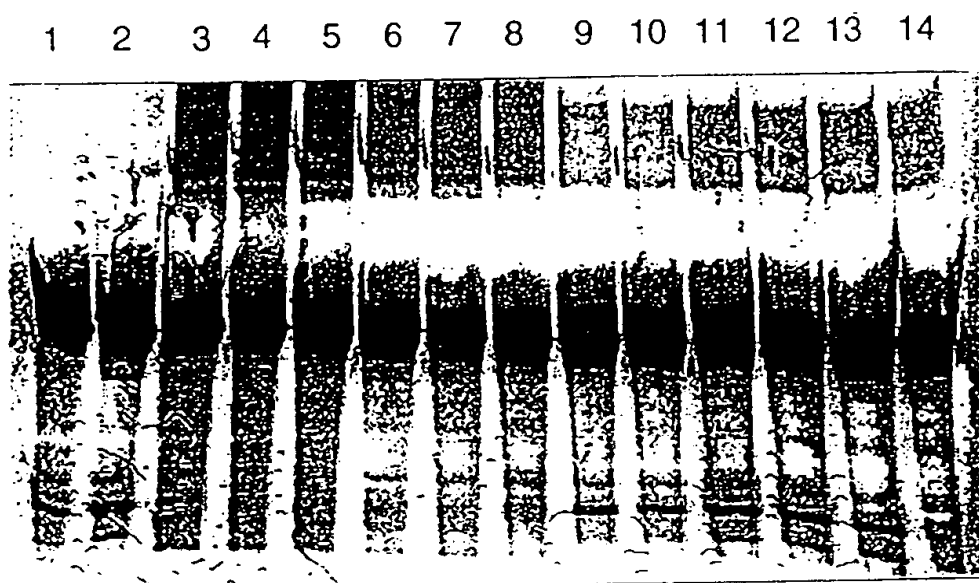


FIG. 44

FOOT" 29928660

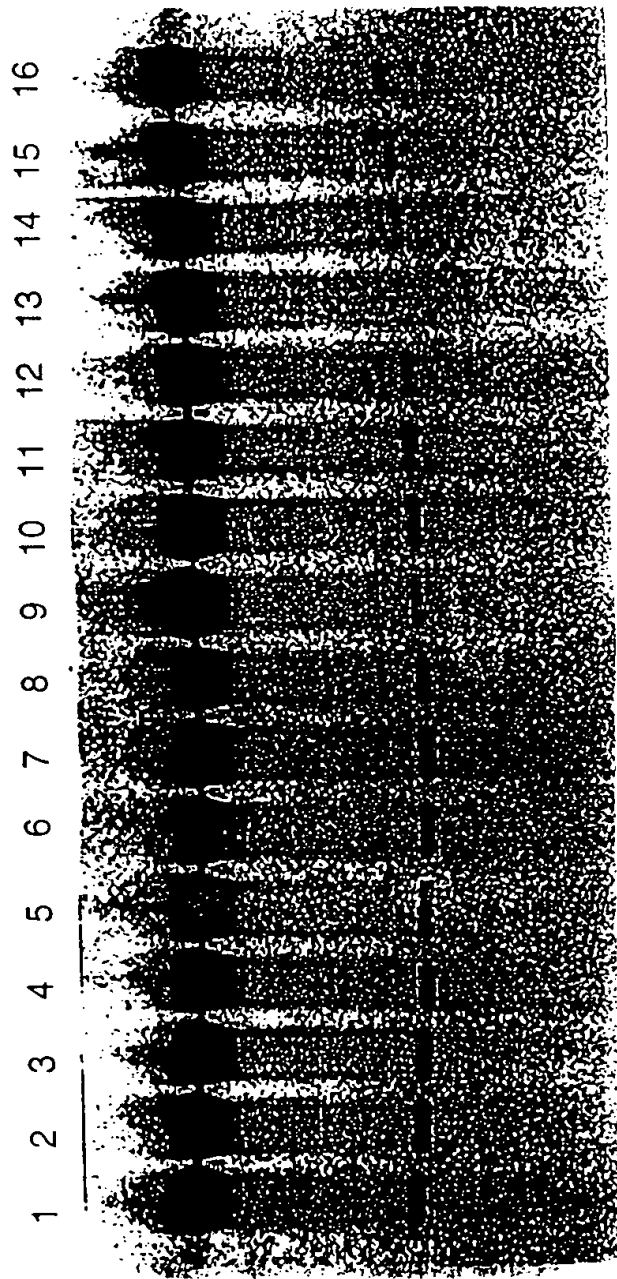


FIG. 45

09982667 "101801

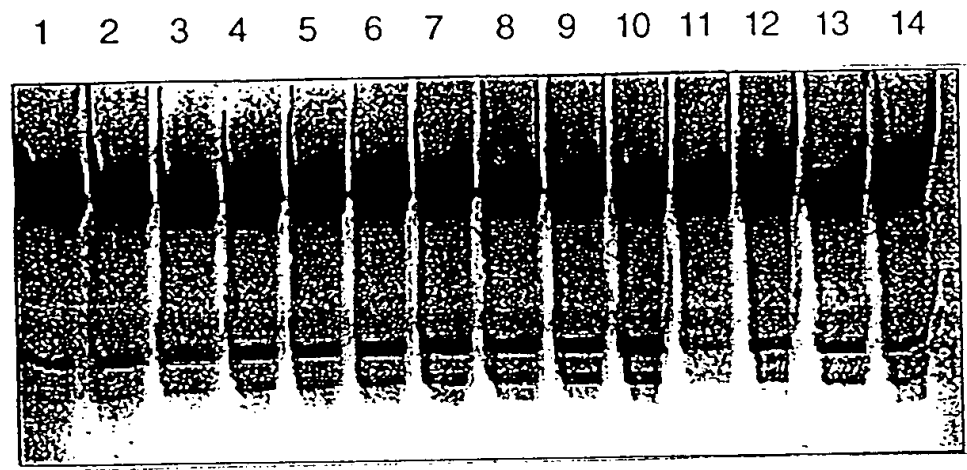


FIG. 46

09982667-101801

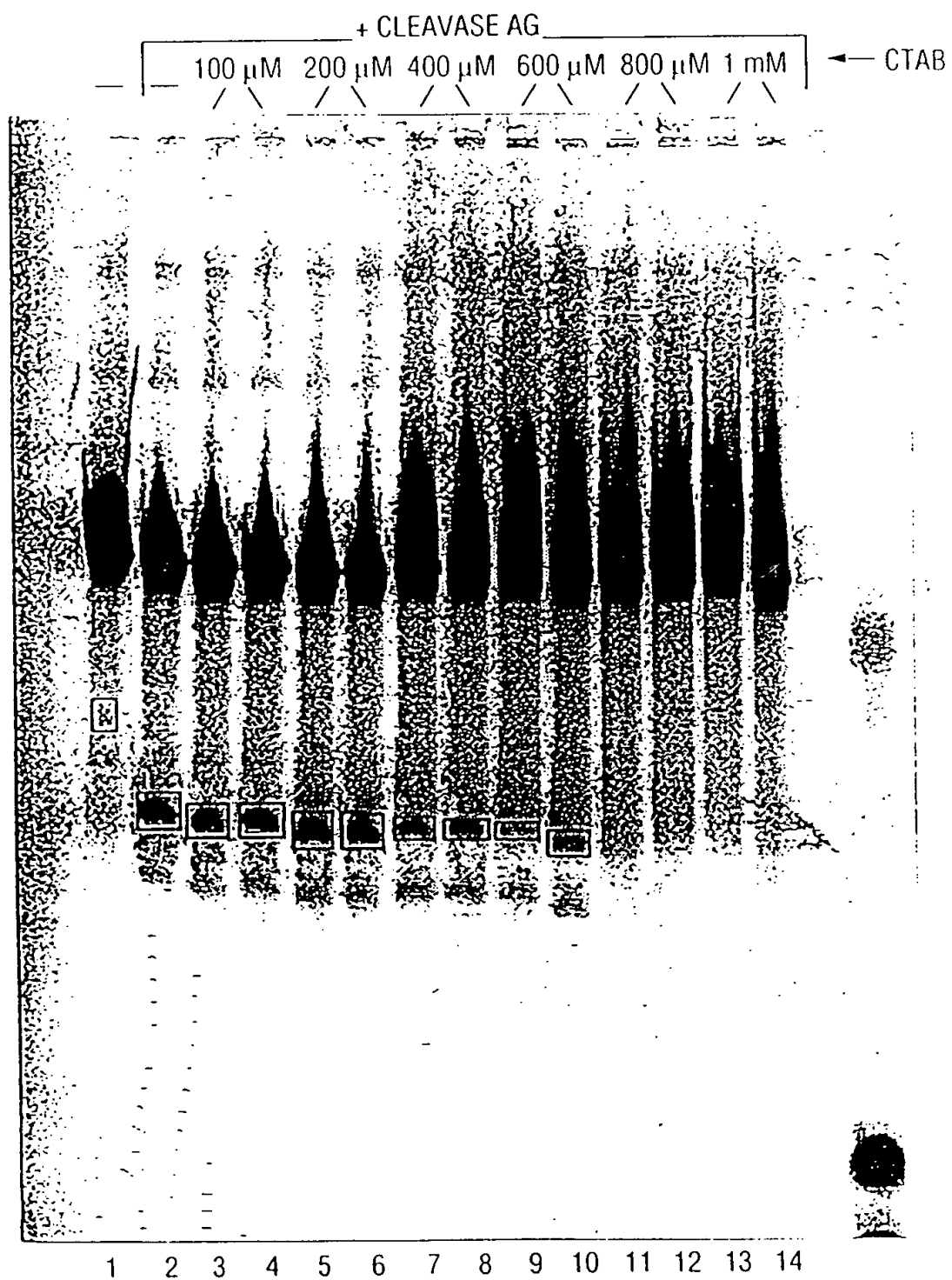


FIG. 47

09982667-101801

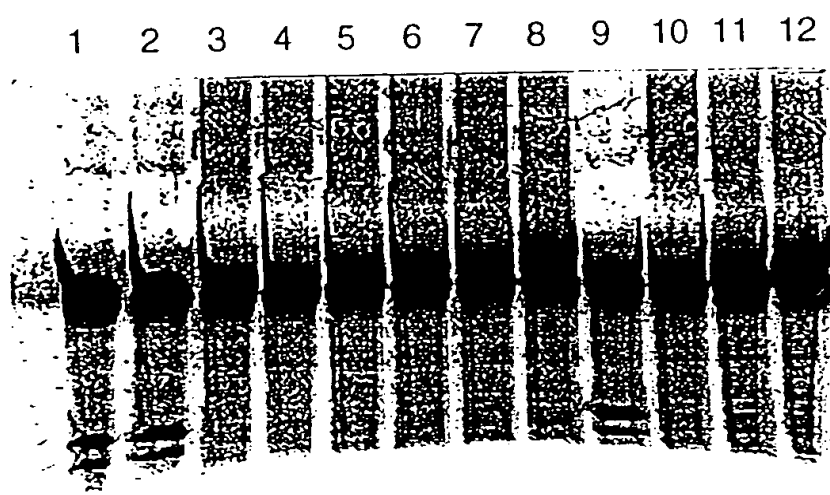


FIG. 48

09982657-101801

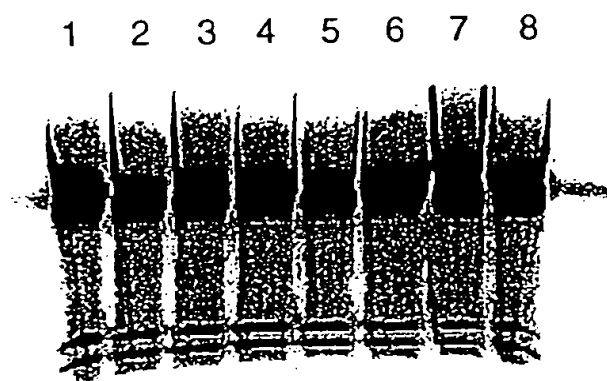


FIG. 49

09982667.101801

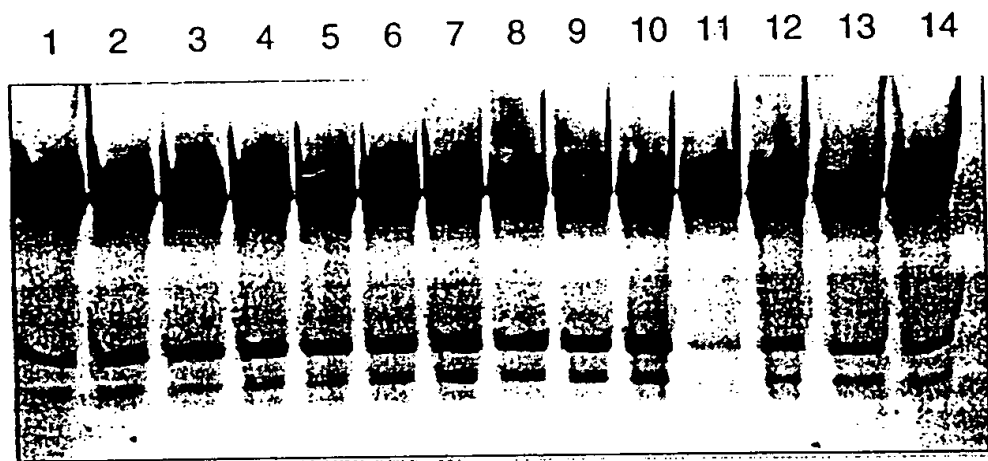


FIG. 50

09982667 "101801

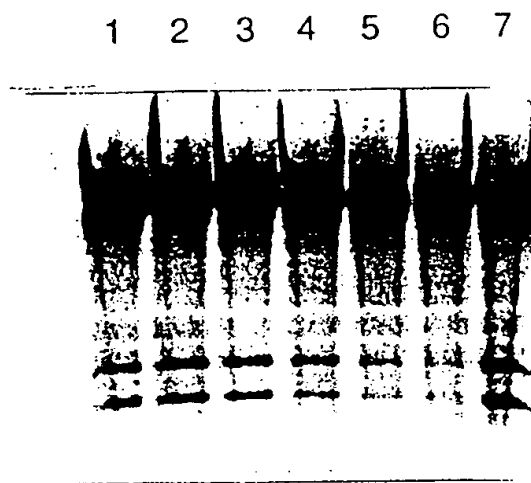


FIG. 51

09982667-101801

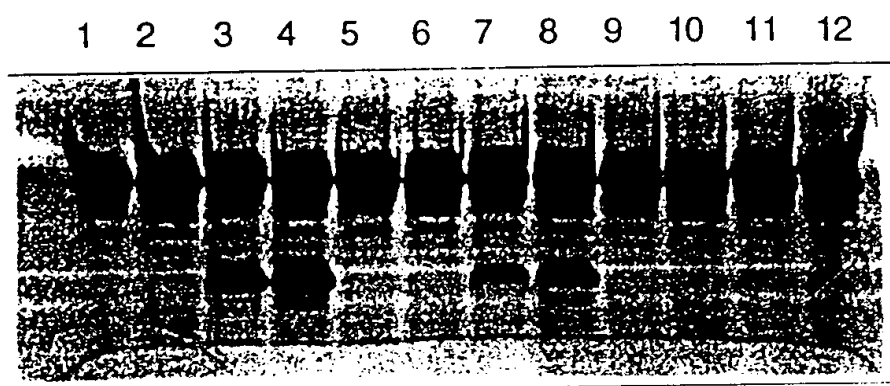


FIG. 52

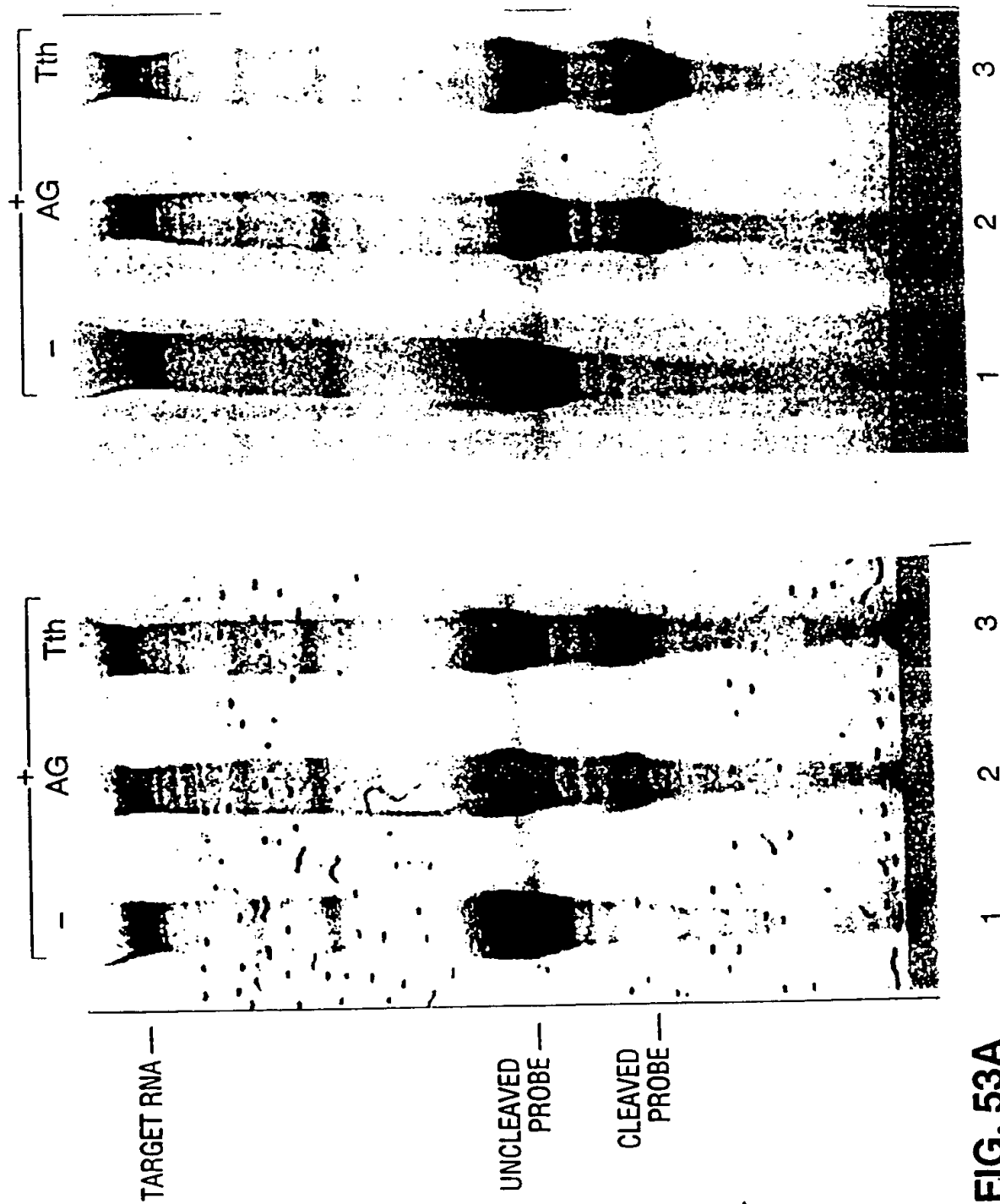


FIG. 53A

FIG. 53B

T08T0T" 29928660

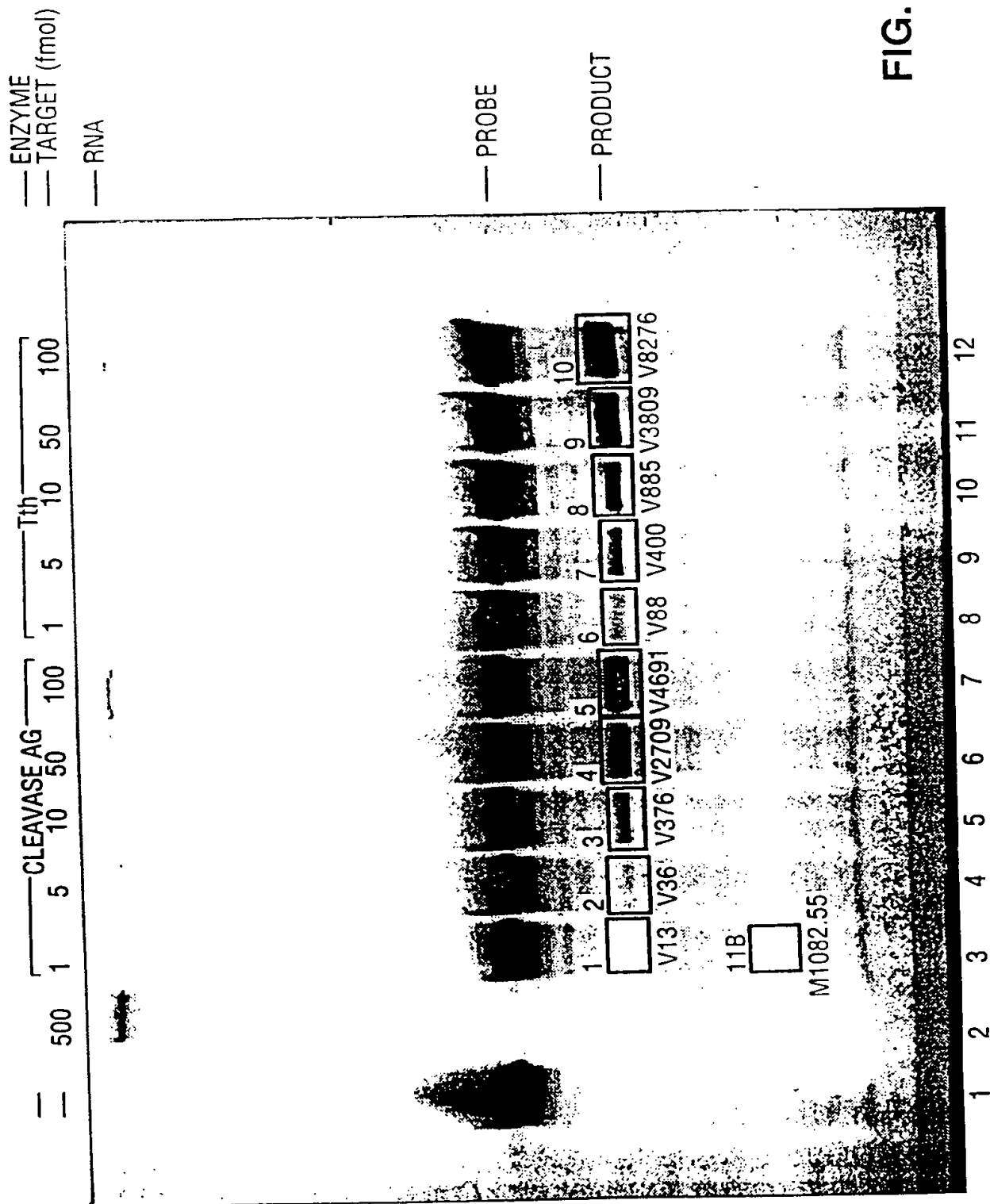


FIG. 54

09982667.101801

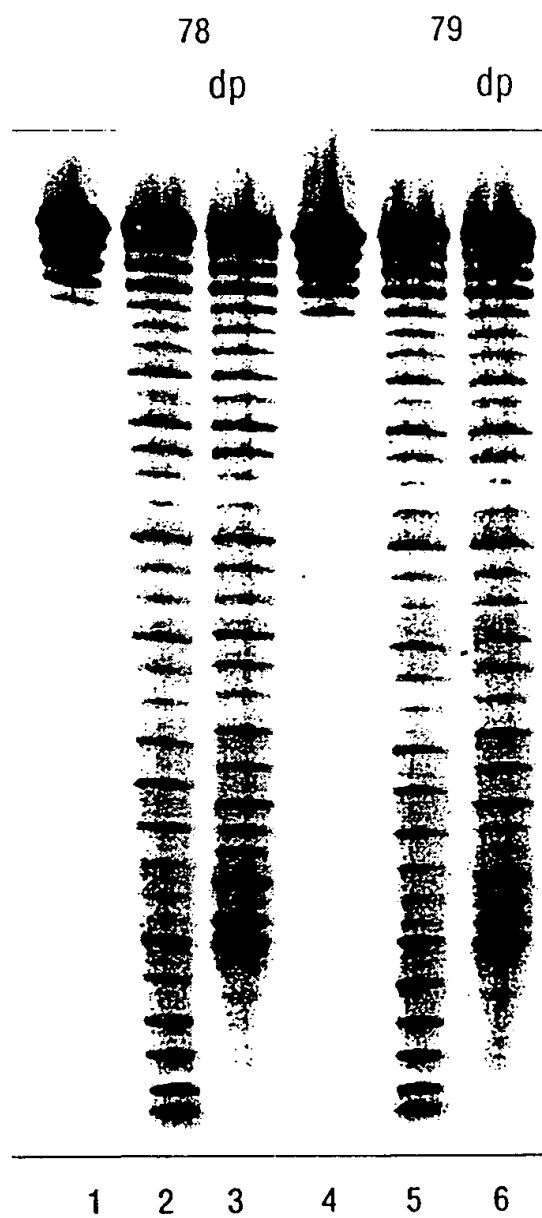


FIG. 55

70 (C10 amino T's)
74 (C6 amino T's)

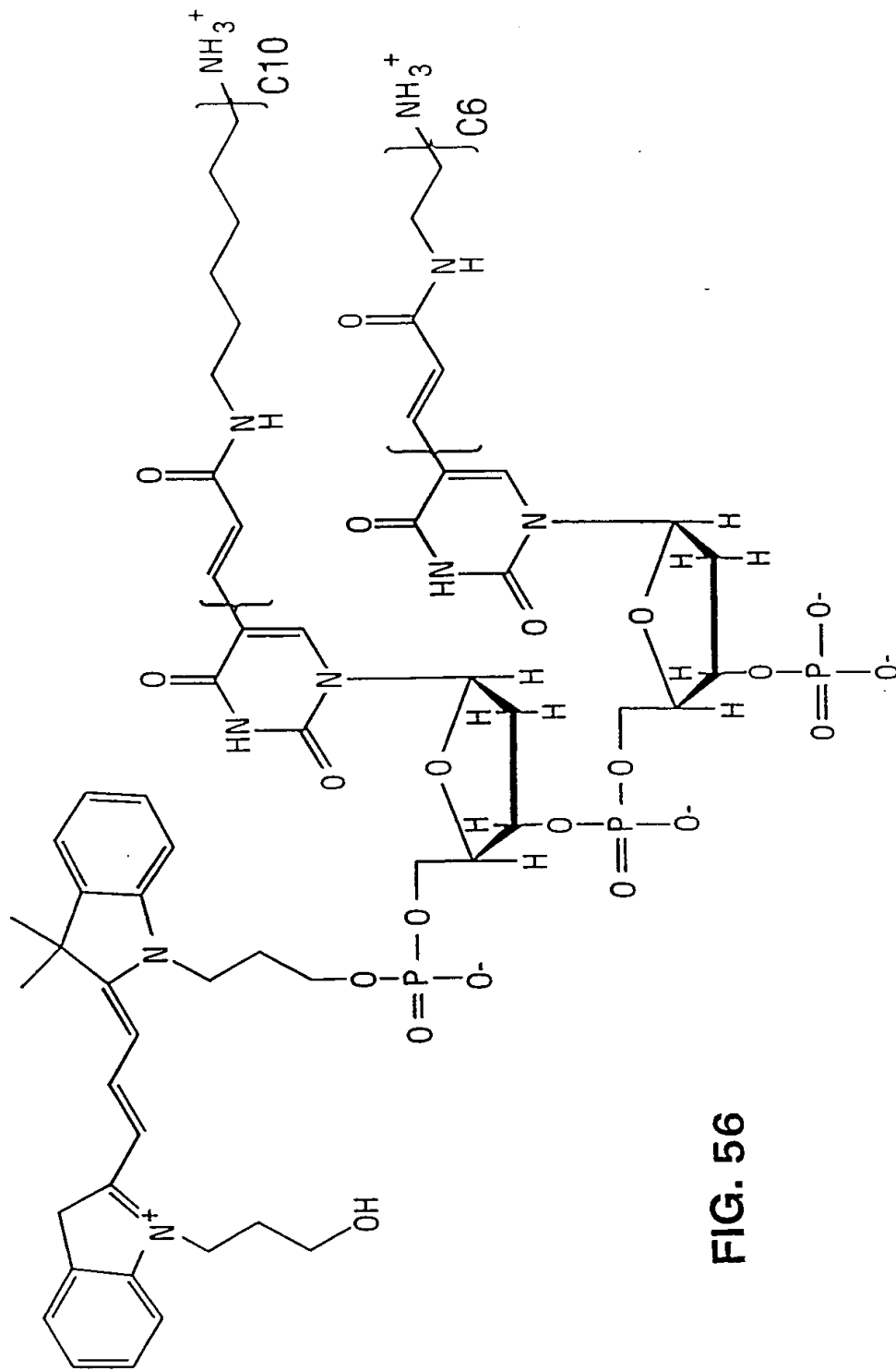


FIG. 56

75

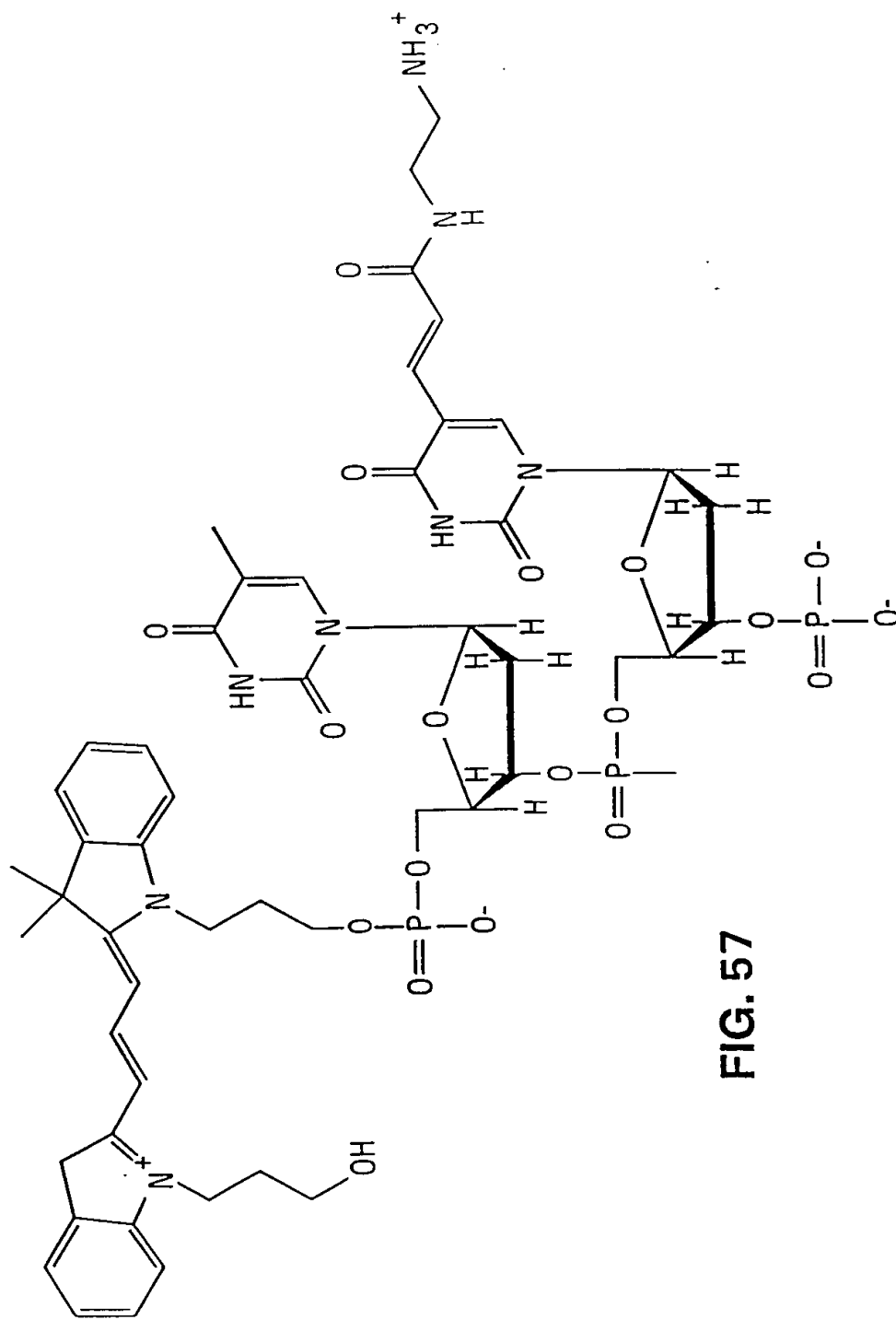


FIG. 57

76

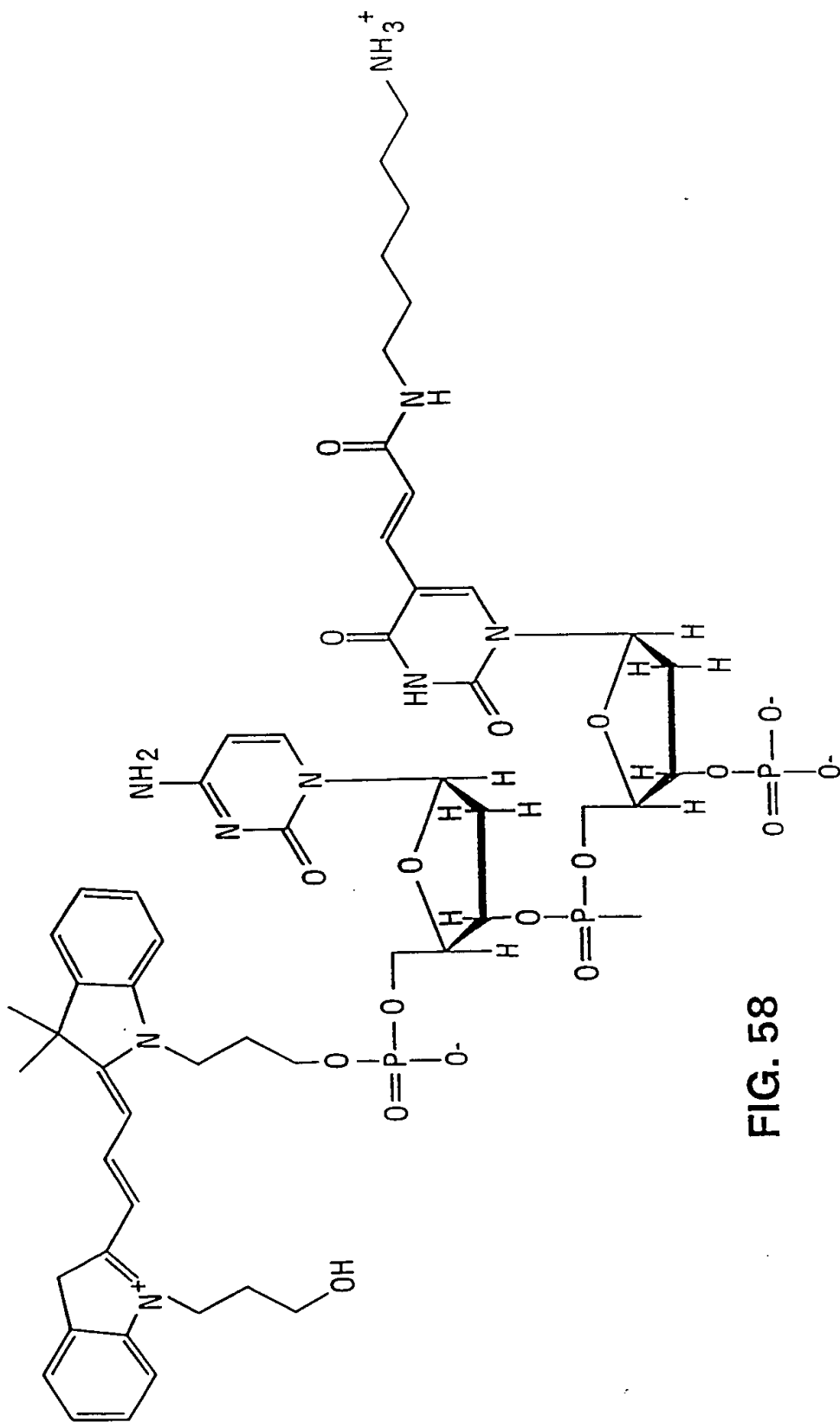


FIG. 58

09982667 . 101801

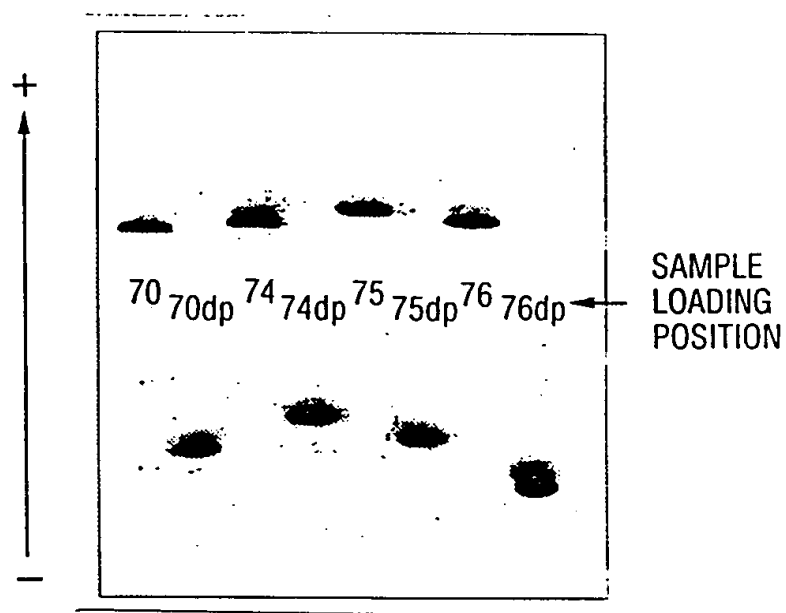


FIG. 59

09982667-101801

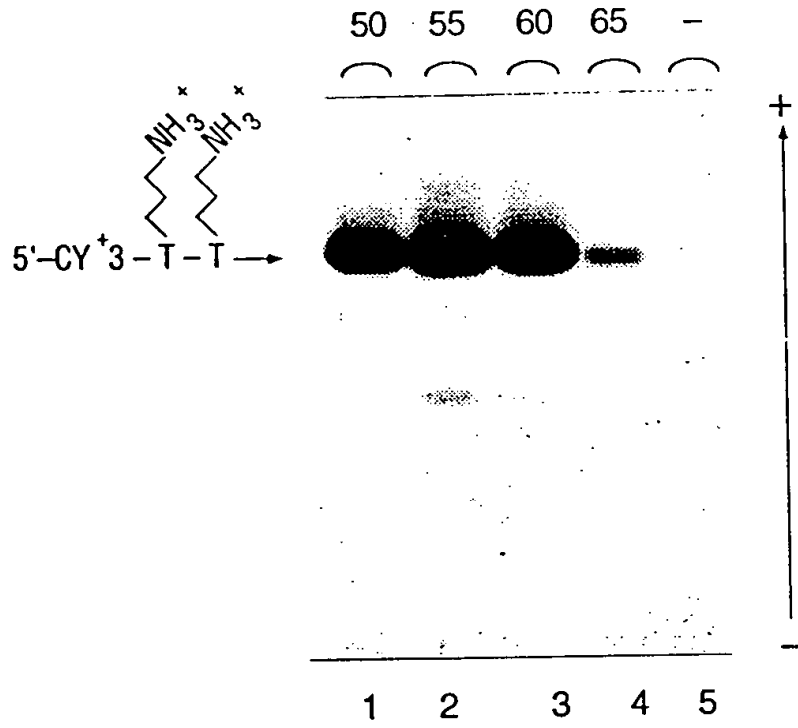


FIG. 60B

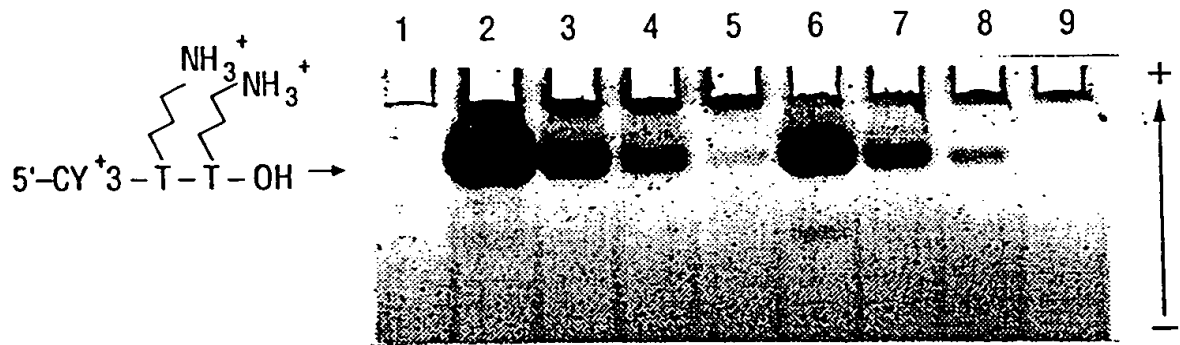


FIG. 61

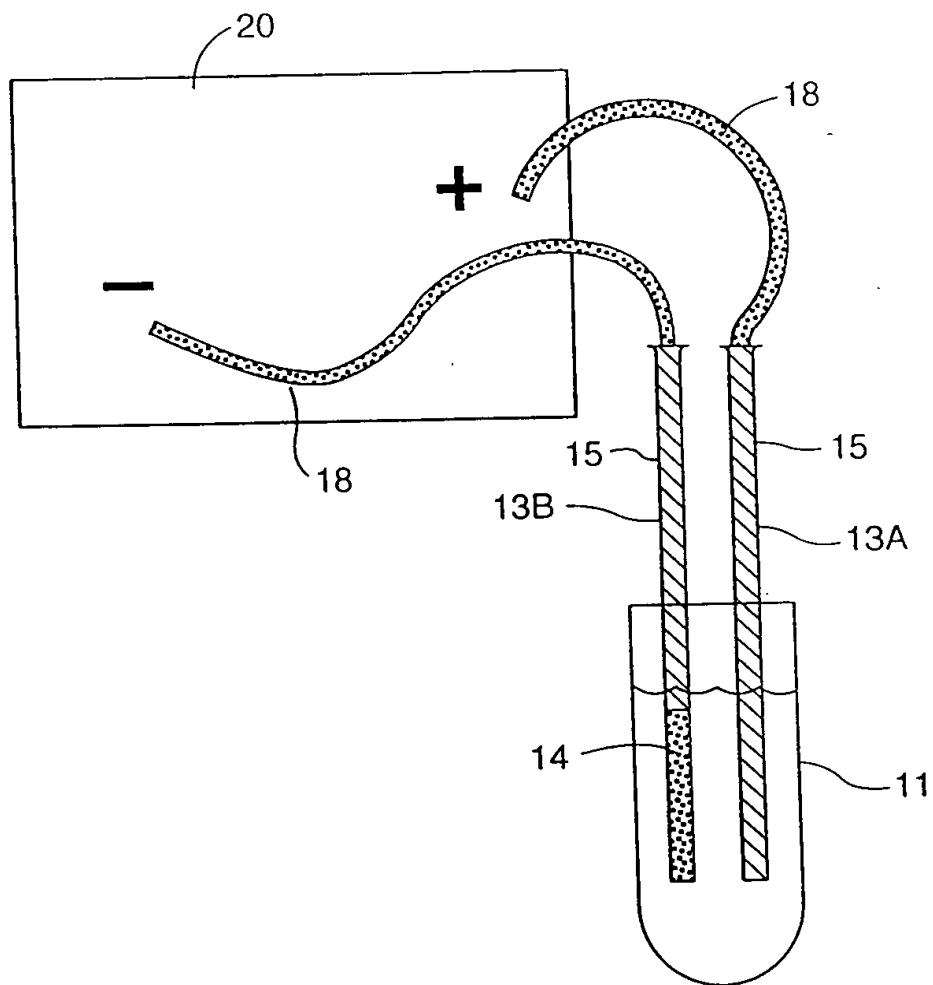


FIG. 62

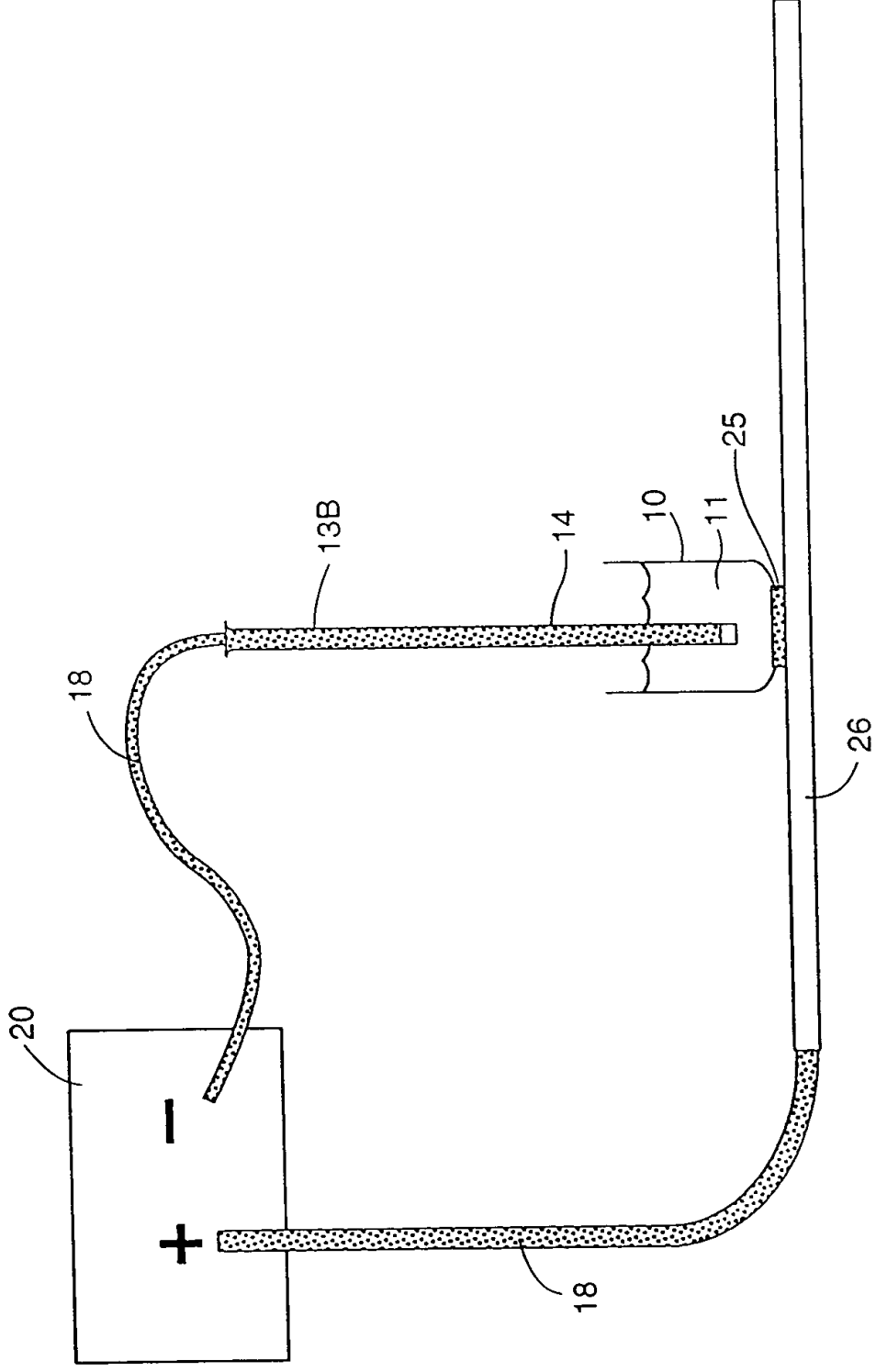


FIG. 63

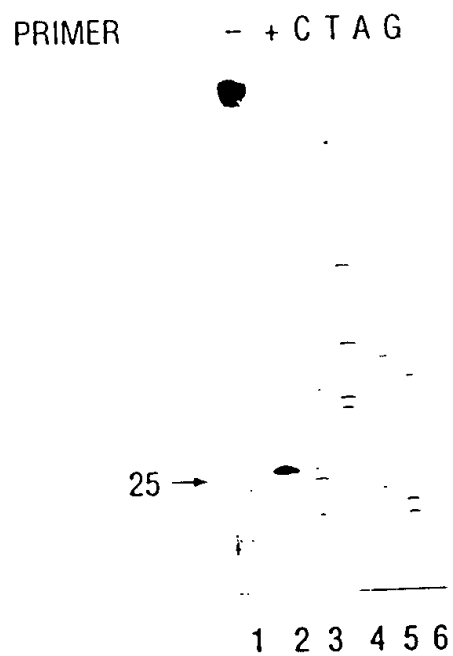


FIG. 64



FIG. 65A



FIG. 65B



FIG. 65C



FIG. 65D

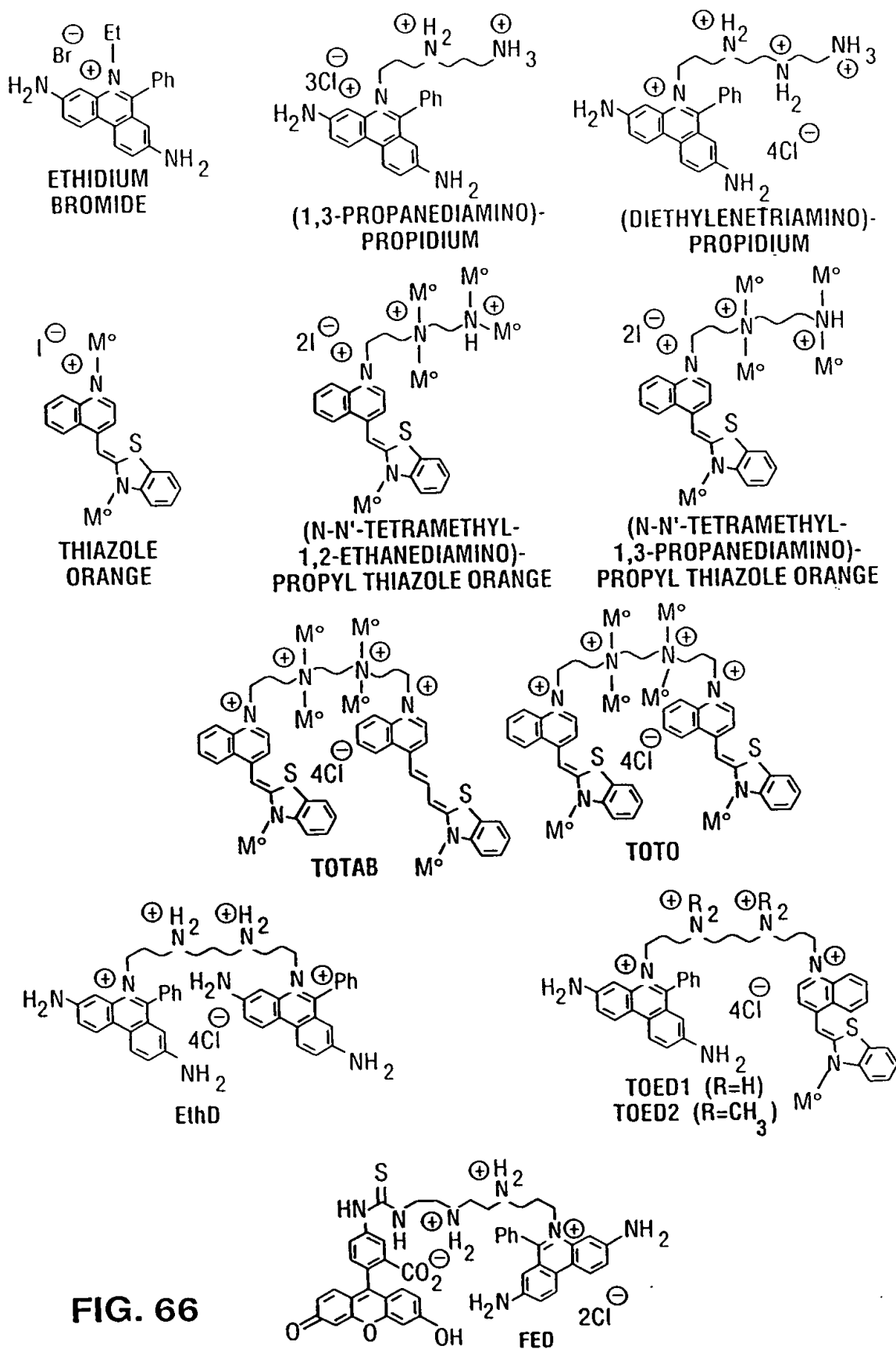


FIG. 66

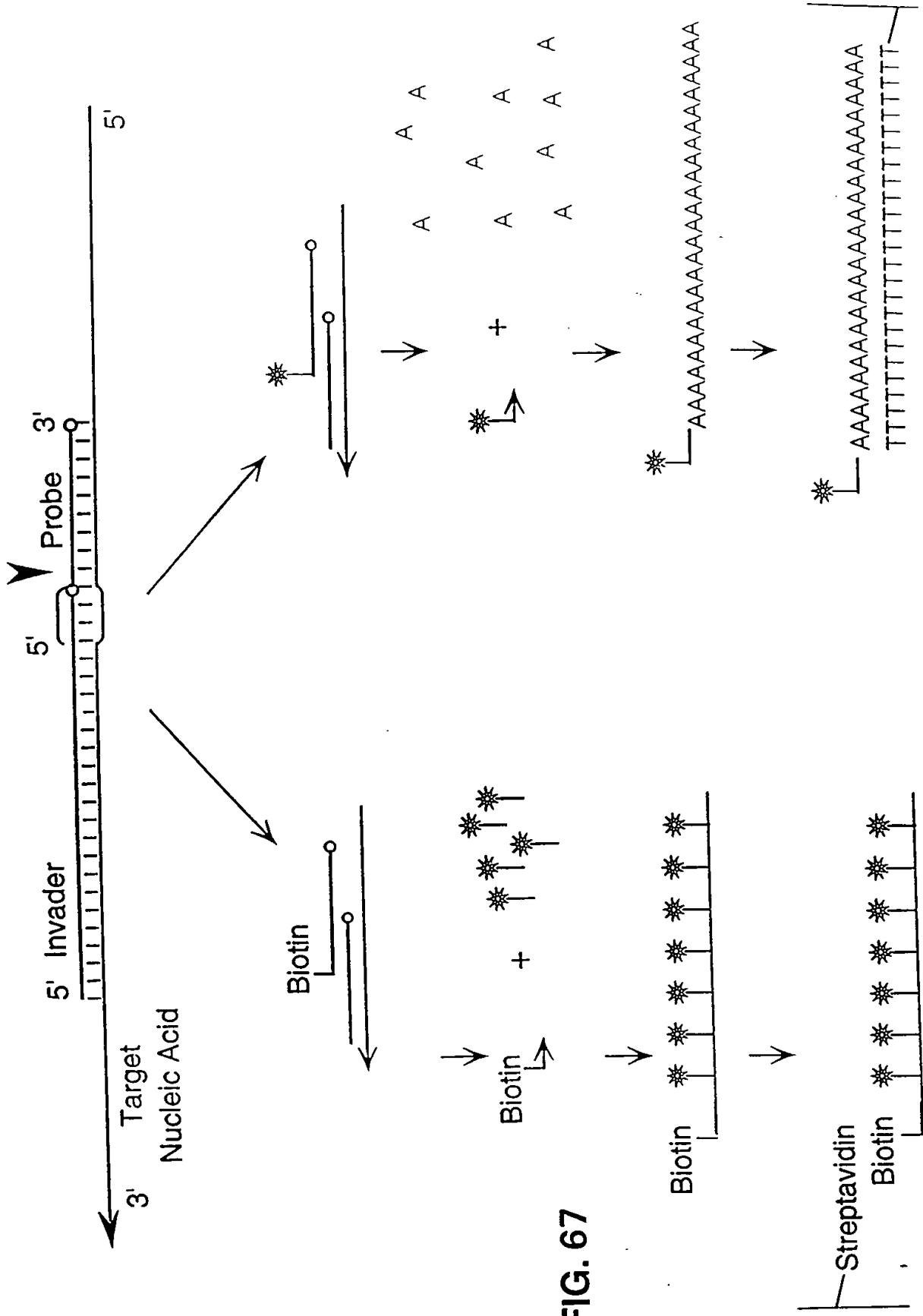


FIG. 67

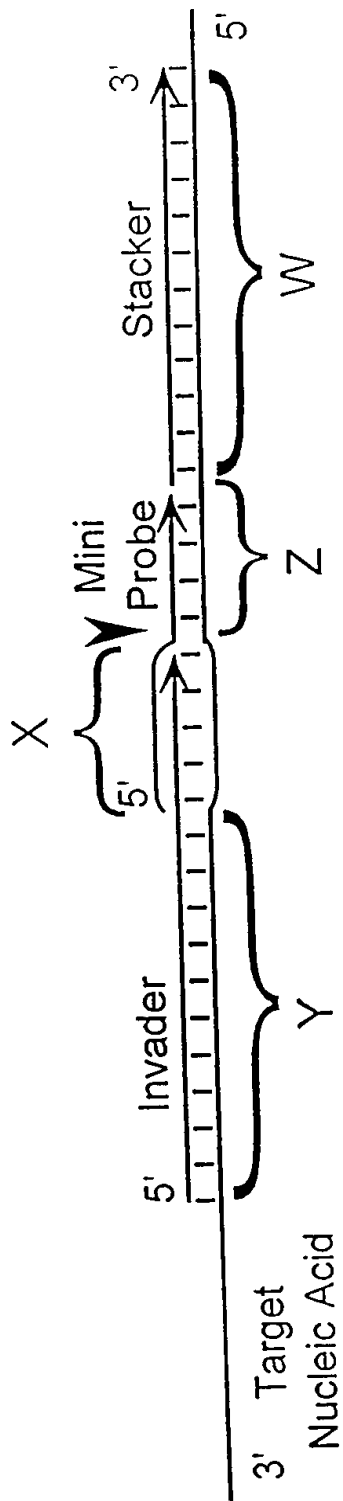


FIG. 68

09982667-101801



FIG. 69

	10	20	30	40	50	60	70
1	MGVQ-----	FGDFIPK--	NIISFEDLKGKKVAIDGMNALYQFLT	SIRLRDGSPLNRKGEITSAYNGVFY	MJAFEN1.PRO		
1	MGVP-----	IGEIIPR--	KEIELENLYGKKIAIDALNAIYQFL	STIRQKDGTPLMDSKGRITSHLSGLFY	PFUFEN1.PRO		
1	MGIQGLAKLI	ADVAPSAI	RENDIKSYFGRKVAIDASMSIYQFL	IAVRQ--GGDVLQNEEGETTSHLMGMFY	HUMFEN1.PRO		
1	MGIHGLAKLI	ADVAPSAI	RENDIKSYFGRKVAIDASMSIYQFL	IAVRQ--GGDVLQNEEGETTS-LMGMFY	MUSFEN1.PRO		
1	MGIKGLNAI	SEHVPSAI	RKSDIKSFFGRKVAIDASMSLYQFL	IAVRQDGGQLTNEAGETTSHLMGMFY	YST510.PRO		
1	MGVHSFWDI	AG-----	PTARPVRL	ESLEDKRM	AVDASIWIYQFLKAVRDQEGNAVKN-----	SHITGFFR	YSTRAD2.PRO
1	MGVSGLWNI	LE-----	PVKRPVKLE	TLVNRKLAID	ASIWIYQFLKAVRDKEGNQLKS-----	SHVVGFFR	SPORAD13.PRO
1	MGVQGLWKL	LE-----	CSGROVS	PEALEGKIL	AVDISIWLNQALKGVRDRHGN	SIEN-----	PHLLTLFH
1	MGVQGLWKL	LE-----	CSGHRVS	PEALEGKVL	AVDISIWLNQALKGVRDSHG	NVN-----	AHLLTLFH
1	MGVQGLWKL	LE-----	CSGRPIN	PGTLEGKIL	AVDISIWLNQAVKGARDRQ	GNAIQN-----	AHLLTLFH
1	MTINGIWE	WANHVV--	--RKVPNET	MRDKT	LSIDGHIWL	YESLKGCEAHHQQT-----	PNSYLVTFFT
1							CELRAD2.PRO
	80	90	100	110	120	130	140
64	KTIHLENDIT	PIWVFDGE	PPKLEK	TRKVRRE	MEKAE	LKMEAIKK----	EDFEEAAKYAKRVSYLTP
64	RTINLMEAGI	KPVYVFDG	EPPEFKK	KELEKR	REAREE	AEEKWREALEK----	GEIEEARKYAQRATRVNE
70	RTIRMMENGI	KPVYVFDG	KPPQLK	SGELAKR	SERRAE	AEKQLQQAQAA----	GAEOEVEKFTKRLVKVTK
69	RTIRM-ENG	IKPVYVFDG	KPPQLK	SGELAKR	SERRAE	AEKQLQQAQEA----	GMEEEVEKFTKRLVKVTK
71	RJLRMIDNGI	KPCYVFDG	KPPDLK	SHELTKR	SSRRVET	EKKLA--EA----	TTELEKMKQERRLVKVS
61	RICKLLYFGI	RPVFDGG	VPVLKRE	TIRQKERR	QKRESAK	STAR	KLALQNGSNDNKRDSDEV
61	RICKLLFFGI	KPVFDGG	APSLK	RQTIQK	RQARRLD	REENATV	TANKLLALQMRHQAMLLKRD
61	RLCKLLFFRI	PIFVDGD	APLLKK	QTLVKKR	RQKDLA	SSDSRKT	TEKLLKTF
61	RLCKLLFFRI	PIFVDGD	APLLKK	QTLVKKR	RQKDLA	SSDSRKT	TEKLLKTF
61	RLCKLLFFRI	PIFVDGD	APLLKK	QTLVKKR	RQKDLA	SSDSRKT	TEKLLKTF
61	RLCKLLFFRI	PIFVDGD	APLLKK	QTLVKKR	RQKDLA	SSDSRKT	TEKLLKTF
61	RIQRLLEKI	PIVVDN	INASSA	HESKDQ	NEFVPR	KRRSFGDS	PFTNLV-----
60							CELRAD2.PRO

FIG. 70A

	150	160	170	180	190	200	210	
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEM----							MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFGAPRLVRNLITGKRKLPGK							PFUFEN1.PRO
136	QHNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ							HUMFEN1.PRO
134	QHNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ							MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTEAEQAELAKKGVYAAASEDMDTLCYRTPFLRLHLTFSEAKKEPIH							YST510.PRO
131	DMIKEVQELLSRFGIPYITAPMEAEQAELQLNLVDGIITDSDVFLFGGKIYKNMFHEKNY---VE							YSTRAD2.PRO
131	VMIKECQELRLFGIPYIVAPOEAEQAQCSKLELKLVDGIVTDDSDVFLFGGTRVYRNMFNQNKF---VE							SPORAD13.PRO
131	QMFLESQELRLFGIPYIQAPMEAEQAQCAILDLDQTSGITDSDIWLFGARHVYRNFNKNKF---VE							HUMXPG.PRO
131	QMFLESQELRLFGIPYIQAPMEAEQAQCAILDLDQTSGITDSDIWLFGARHVYRNFNKNKF---VE							MUSXPG.PRO
131	QMCLESQELQLFGIPYIVAPMEAEQAQCAILDLDQTSGITDSDIWLFGARHVYRNFNKNKF---VE							XENXPG.PRO
111	DHVKYKTNALLTELGIKVIAPGDGEAQCARLEQLGVTSGCITTDYFLFGGKNLYRFDFTAGT-----							CELRAD2.PRO
	220	230	240	250	260	270	280	
195	-----PELIELNEVLEDLRISLDDLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV							MJAFEN1.PRO
200	NVYVE-IKPELIILEEVLKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF							PFUFEN1.PRO
206	EFHLSRIQLQELGLNQEQQFVDCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN-----KY							HUMFEN1.PRO
204	EFHLSRVLQELGLNQEQQFVDCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS-----KY							MUSFEN1.PRO
204	EIDTELVLRLGLDLTIEQFVDCIMLGCDYCESIRGVGPVTALKIKT--HGSIEKIVEFIESGESNNTKW							YST510.PRO
198	FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNNGOFDKRK							YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLGSDYTMGLSRVGPVLALEILHEFPDGTGLFEKKWFQRLSTGHAS							SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPBGHLEPLLKFSWWHEAQKNP							HUMXPG.PRO
119	YYQYVDFYSQLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPBGRLDPLLKFSWWHEAQNNK							MUSXPG.PRO
198	YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPTVGYVSAMEILNEFPGQGLEPLVKFKEWWSEAQKDK							XENXPG.PRO
175	-----SSTACLDHIMHLSLGRMFM-----							CELRAD2.PRO

FIG. 70B

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKRIFKEPKV-----	TD--NYSLSLKLDPKEGIIKFLVDENDFNYD	MJAFEN1.PRO				
265	QKQSDVDLYAIKEFFLNPPV-----	TD--NYNLVWRDPDEEGILKFLCDEHDFSEE	PFUFEN1.PRO				
269	PVPENWLHKEAHQLFLEPEV-----	LDPESELKWSEPNEEEELKFCMCGEKQFSEE	HUMFEN1.PRO				
267	PVPENWLHKEAQQLFLEPEV-----	VDPESELKWSEPNEEEELVKFCMCGEKQFSEE	MUSFEN1.PRO				
272	KIPEDWPYKQARMFLDPEV-----	IDGNEINLKWSPPKKEKELIEYLCDDKKFSEE	YST510.PRO				
265	QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDMLRSFMKTQLGWPHE	YSTRAD2.PRO					
268	KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGIPDLDELRLQFLMATVGWSKQ	SPORAD13.PRO					
268	KIRPNPHDTKVKKKL--RTLQLTPGFPNPAVAEAYLKPVVDDSKGSFLWGKPDLDKIREFCQRYFGWNRT	HUMXPG.PRO					
268	KVAENPYDTKVKKKL--RKLQLTPGFPNPAVADAYLRPVVDDSRGSFLWGKPDVDKIREFCORYFGWNRM	MUSXPG.PRO					
268	KMRPNPNDTKVKKKL--RLDLQSQFPNPAVASAYLKPVVDESKSAFSWGRPDLEQIREFCESRFGWYRL	XENXPG.PRO					
194	-----EKKVSRPHLITAILLGCDYFORGVQNIIGIVSVFD-ILGEFGDDGNEEIDPHVILDRFASYVRE	CELRAD2.PRO					
	360	370	380	390	400	410	420
300	RVKKHVDKLYNLIA-----						MJAFEN1.PRO
314	RVKNGLERLKKAI-----						PFUFEN1.PRO
320	RIRSGVKRLSKSRQGS-TQGRLDFFKVT-----						HUMFEN1.PRO
318	RIRSGVKRLSKSRQGS-TQGRLDFFKVT-----						MUSFEN1.PRO
323	RVKSGISRLKGLKSG-IQGRLDGFFOVV-----						YST510.PRO
335	KSDEILIPLIRDVNKRKK-----						YSTRAD2.PRO
337	RTNEVLLPVIQDMHKKOF-----						SPORAD13.PRO
336	KTDESILFPVLKQLDAQQTQLRIDSFFRLAQKEKEDAKRIKSQRLNRAVTCMLRKEKEAASEIEAVSVAM						HUMXPG.PRO
336	KTDESILYPVLKHLNAHQTLRIDSFFRLAQKEKQDAKLKSHRLSRAVTCMLRKEREKAPELTKVTEAM						MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQTQLRIDSFFRLAQHEAAG--LKSQRLRAVTCMKRKERDVEAEVEAAVAM						XENXPG.PRO
257	EIPARSEDTRKRLRLRRKKYNFPVGFPCNDAVHNAITMYLRPPVSSEIPKIIPR-----						AANFQQVAEIM CELRAD2.PRO

FIG. 70C

	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----	YST510.PRO
357	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
406	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
406	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
403	-----	-----	-----	-----	-----	-----	XENXPG.PRO
322	-----	-----	-----	-----	-----	-----	CELRAD2.PRO
314	-----	-----	-----	-----	-----	-----	NKTKQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	-----	-----	-----	-----	-----	-----	KKKAKTGAAG HUMFEN1.PRO
350	-----	-----	-----	-----	-----	-----	KKKAKTGGAG MUSFEN1.PRO
354	-----	-----	-----	-----	-----	-----	NKKNKNKNK YST510.PRO
364	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
429	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
476	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
469	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
458	-----	-----	-----	-----	-----	-----	XENXPG.PRO
387	-----	-----	-----	-----	-----	-----	CELRAD2.PRO

FIG. 70D

TOBTOT" 49928660

MJAFEN1. PRO
PFUFEN1. PRO
HUMFEN1. PRO
MUSFEN1. PRO
YST510. PRO
YSTRAD2. PRO
SPORAD13. PRO
HUMXPG. PRO
MUSXPG. PRO
XENXPG. PRO
CELRAD2. PRO

322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 ---RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

FIG. 70E

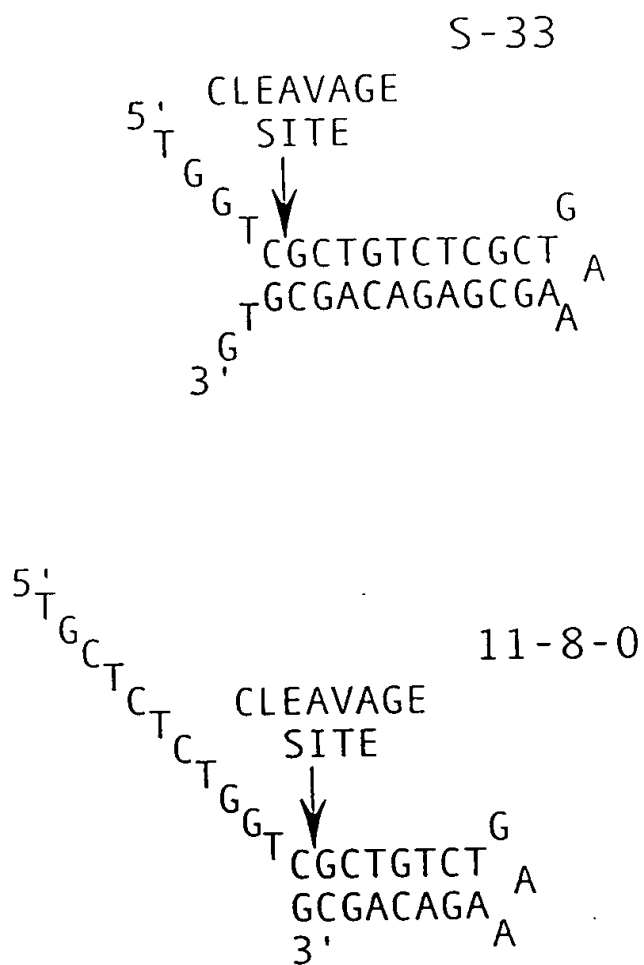


FIG. 71